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(54) Title: NUCLEIC ACIDS ENCODING <i>TAXUS</i> GERANYLGERANYL DIPHOSPHATE SYNTHASE, AND METHODS OF USE (57) Abstract <p>A cDNA encoding geranylgeranyl diphosphate synthase from Canadian Yew (<i>Taxus canadensis</i>) has been isolated and sequenced, and the corresponding amino acid sequence has been determined. Accordingly, an isolated DNA sequence (SEQ NO:1) is provided which codes for the expression of geranylgeranyl diphosphate synthase (SEQ ID NO:2), from Canadian Yew (<i>Taxus canadensis</i>). In other aspects, replicable recombinant cloning vehicles are provided which code for geranylgeranyl diphosphate synthase, or for a base sequence sufficiently complementary to at least a portion of geranylgeranyl diphosphate synthase DNA or RNA to enable hybridization therewith. In yet other aspects, modified host cells are provided that have been transformed, transfected, infected and/or injected with a recombinant cloning vehicle and/or DNA sequence encoding geranylgeranyl diphosphate synthase. Thus, systems and methods are provided for the recombinant expression of the aforementioned recombinant geranylgeranyl diphosphate synthase that may be used to facilitate its production, isolation and purification in significant amounts. Recombinant geranylgeranyl diphosphate synthase may be used to obtain expression or enhanced expression of geranylgeranyl diphosphate synthase in plants in order to enhance the production of geranylgeranyl diphosphate, or diterpenes derived therefrom, or may be otherwise employed for the regulation or expression of geranylgeranyl diphosphate synthase, or the production of its products.</p>		

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**NUCLEIC ACIDS ENCODING *TAXUS* GERANYLGERANYL
DIPHOSPHATE SYNTHASE, AND METHODS OF USE**

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5 The government has certain rights in this invention.

Field of the Invention

This invention relates to nucleic acid sequences encoding geranylgeranyl diphosphate synthase, in particular to nucleic acid sequences encoding geranylgeranyl diphosphate synthase from yew.

10 Background of the Invention

The diterpenoid anti-cancer drug paclitaxel and related taxanes accumulate in resin cells of *Taxus* (yew) stem, needle and root tissue (Croom, E.M., Jr. (1995) in *Taxol: Science and Applications* (Suffness, M., Ed.), pp. 37-70, CRC Press, Boca Raton, FL.), and in cell cultures of yew (Ketchum, R.E.B. and Gibson, D.M. (1996) *Plant Cell Tiss. Org. Cult.*, 46:9-16; Christen, A.A. et al (1989) *Proc. Am. Assoc. Cancer Res.*, 30:566 [See also U.S. Patent No. 5,019,504]) in which production is induced by methyl jasmonate (Yukimune, Y., Tabata, H., Higashi, M. and Hara, Y. (1996) *Nature Biotech.*, 14:1129-1132; Ketchum, R.E.B., Gibson, D.M., Croteau, R.B. and Shuler, M.L. (1998) *Biotech. Bioeng.*, in press). Paclitaxel has been
15 approved for treatment of refractory ovarian and metastatic breast cancer and, more recently, for small cell lung cancer (Rose, W.C. (1995) in *Taxol: Science and Applications* (Suffness, M., Ed.), pp. 209-236, CRC Press, Boca Raton, FL.), and ongoing clinical trials suggest expanded applications in cancer chemotherapy, both in
20 treatment of additional cancer types and in use much earlier in the course of

intervention (Holmes, F.A., Kudelka, A.P., Kavanagh, J.J., Huber, M.H., Ajani, J.A. and Valero, V. (1995) in *Taxane Anticancer Agents: Basic Science and Current Status* (Georg, G.I., Chen, T.T., Ojima, I. and Vyas, D.M., Eds.), pp. 31-57, American Chemical Society, Washington, DC). The supply and cost of the drug
5 therefore remain important issues (Suffness, M. (1995) in *Taxane Anticancer Agents: Basic Science and Current Status* (Georg, G.I., Chen, T.T., Ojima, I. and Vyas, D.M., Eds.), pp. 1-17, American Chemical Society, Washington, DC).

Paclitaxel has been prepared by total synthesis (Nicolaou, K.C., Yang, Z., Liu, J.J., Ueno, H., Nantermet, P.G., Guy, R.K., Claiborne, C.F., Renaud, J.,
10 Couladouros, E.A., Paulvannin, K. and Sorensen, E.J. (1994) *Nature*, **367**:630-634; Holton, R.A., Kim, H.B., Somoza, C., Liang, F., Biediger, R.J., Boatman, P.D., Shindo, M., Smith, C.C., Kim, S., Nadizadeh, H., Suzuki, Y., Tao, C., Vu, P., Tang, S., Zhang, P., Murthi, K.K., Gentile, L.N. and Liu, J.H. (1994) *J. Am. Chem. Soc.*, **116**:1599-1600; Masters, J.J., Link, J.T., Snyder, L.B., Young, W.B. and
15 Danishefsky, S.J. (1995) *Angew. Chem. Int. Ed. Engl.*, **34**:1723-1726.); however, the synthetic routes are long, expensive, and too low yielding to be commercially useful (Borman, S. (1994) *Chem. Eng. News*, **72**:32-34), and it is clear that, for the foreseeable future, the supply of this drug must continue to rely on biological methods of production (Suffness, M. (1995) in *Taxane Anticancer Agents: Basic Science and*
20 *Current Status* (Georg, G.I., Chen, T.T., Ojima, I. and Vyas, D.M., Eds.), pp. 1-17, American Chemical Society, Washington, DC). It is therefore essential to understand the biosynthesis of paclitaxel, particularly the rate-limiting steps of the pathway, since the manipulation of these slow steps can be expected to lead to improved yield and to the production of the drug in large quantities at reasonable cost.

25 Paclitaxel is formed by the cyclization of the universal diterpenoid precursor geranylgeranyl diphosphate (West, C.A., Dudley, M.W. and Dueber, M.T. (1979) *Recent Adv. Phytochem.*, **13**:163-198; West, C.A. (1981) in *Biosynthesis of Isoprenoid Compounds* (Porter, J.W. and Spurgeon, S.L., Eds.), Vol. 1, pp. 375-411, Wiley, New York, NY; Gershenzon, J. and Croteau, R. (1993) in *Lipid Metabolism in*
30 *Plants* (Moore, T. S., Jr., Ed.), pp. 339-388, CRC Press, Boca Raton, FL.) to taxadiene (Koepp, A.E., Hezari, M., Zajicek, J., Stofer Vogel, B., LaFever, R.E., Lewis, N.G. and Croteau, R. (1995) *J. Biol. Chem.*, **270**:8686-8690) to establish the taxane skeleton, which then undergoes extensive oxidative modification and-addition of side chains (Hezari, M. and Croteau, R. (1997) *Planta Med.*, **63**:291-
35 295) (FIGURE 1). The properties and mechanism of taxadiene synthase have been

- examined in some detail (Hezari, M., Lewis, N.G. and Croteau, R. (1995) *Arch. Biochem. Biophys.*, **322**:437-444; Lin, X., Hezari, M., Koepp, A.E., Floss, H.G. and Croteau, R. (1996) *Biochemistry*, **35**:2968-2977), the corresponding cDNA has been cloned (Wildung, M.R. and Croteau, R. (1996) *J. Biol. Chem.*, **271**:9201-9204), and several of the subsequent cytochrome P450-catalyzed hydroxylations (Hezari, M. and Croteau, R. (1997) *Planta Med.*, **63**:291-295; Hefner, J., Rubenstein, S.M., Ketchum, R.E.B., Gibson, D.M., Williams, R.M. and Croteau, R. (1996) *Chem. Biol.*, **3**:479-489) and acylation steps (Zocher, R., Weckwerth, W., Hacker, C., Kammer, B., Hornbogen, T. and Ewald, D. (1996) *Biochem. Biophys. Res. Commun.*, **229**:16-20) of the pathway have been demonstrated.

- Genes encoding GGPP synthase are of interest because this branch point prenyltransferase (West, C.A., Dudley, M.W. and Dueber, M.T. (1979) *Recent Adv. Phytochem.*, **13**:163-198; West, C.A. (1981) in *Biosynthesis of Isoprenoid Compounds* (Porter, J.W. and Spurgeon, S.L., Eds.), Vol. 1, pp. 375-411, Wiley, New York, NY; Gershenzon, J. and Croteau, R. (1993) in *Lipid Metabolism in Plants* (Moore, T.S., Jr., Ed.), pp. 339-388, CRC Press, Boca Raton, FL.) provides the substrate for protein prenylation (Rilling, H.C., Breunger, E., Epstein, W.W. and Crain, P.F. (1989) *Science*, **247**:318-320; Clarke, S. (1992) *Annu. Rev. Biochem.*, **61**:355-386.), the formation of the phytol moiety of chlorophylls (Kleinig, H. (1989) *Annu. Rev. Plant Physiol. Plant Mol. Biol.*, **40**:39-59), side-chain syntheses of prenylated quinones and tocopherols (Schultz, G., Soll, J., Fiedler, E. and Schulze-Siebert, D. (1985) *Physiol. Plant.*, **64**:123-129), the production of carotenoid pigments (Chappell, J. (1995) *Plant Physiol.*, **107**:1-6; Bonk, M., Hoffman, B., Von Lintig, J., Schledz, M., Al-Babili, S., Hobeika, E., Kleinig, H. and Beyer, P. (1997) *Eur. J. Biochem.*, **247**:942-950; Bartley, G.E. and Scolnik, P.A. (1994) *Annu. Rev. Plant Physiol. Plant Mol. Biol.*, **45**:287-301; Bartley, G.E. and Scolnik, P.A. (1995) *Plant Cell*, **7**:1027-1038.) and gibberellin plant hormones (Sun, T. and Kamiya, Y. (1994) *Plant Cell*, **6**:1509-1518), as well as for the biosynthesis of diterpenoid natural products, such as casbene (Dudley, M.W., Green, T.R. and West, C.A. (1986) *Plant Physiol.*, **81**:343-348), oryzalexins (West, C.A., Lois, A.F., Wickham, K.A. and Ren, Y.-Y. (1990) *Recent Adv. Phytochem.*, **24**:219-248) and paclitaxel (Koepp, A.E., Hezari, M., Zajicek, J., Stofer Vogel, B., LaFever, R.E., Lewis, N.G. and Croteau, R. (1995) *J. Biol. Chem.*, **270**:8686-8690). Since GGPP synthase controls the rate of production of the branch point precursor of paclitaxel, and other useful diterpenes,

there exists a need for methods of enhancing the production of GGPP synthase in cells and tissues that produce paclitaxel and other useful diterpenes.

Summary of the Invention

In accordance with the foregoing, a cDNA encoding geranylgeranyl diphosphate synthase (GGPP synthase) from Canadian Yew (*Taxus canadensis*) has been isolated and sequenced, and the corresponding amino acid sequence has been deduced. Accordingly, the present invention relates to isolated DNA sequences which code for the expression of geranylgeranyl diphosphate synthase, such as the sequence designated SEQ ID NO:1 which encodes a geranylgeranyl diphosphate synthase (GGPP synthase) protein (SEQ ID NO:2) from Yew (*Taxus canadensis*). Additionally, the present invention relates to isolated, recombinant geranylgeranyl diphosphate synthase (GGPP synthase) protein from Yew (*Taxus canadensis*). In other aspects, the present invention is directed to replicable recombinant cloning vehicles comprising a nucleic acid sequence, e.g., a DNA sequence which codes for a geranylgeranyl diphosphate synthase, or for a base sequence sufficiently complementary to at least a portion of DNA or RNA encoding geranylgeranyl diphosphate synthase to enable hybridization therewith (e.g., antisense RNA or fragments of DNA complementary to a portion of DNA or RNA molecules encoding geranylgeranyl diphosphate synthase which are useful as polymerase chain reaction primers or as probes for geranylgeranyl diphosphate synthase or related genes). In yet other aspects of the invention, modified host cells are provided that have been transformed, transfected, infected and/or injected with a recombinant cloning vehicle and/or DNA sequence of the invention. In yet other aspects of the invention, nucleic acid molecules are provided that are useful as hybridization probes for identifying genes encoding geranylgeranyl diphosphate synthase proteins from microorganisms, such as *Taxomyces andreanae* and *Penicillium raistrickii*. Thus, the present invention provides for the recombinant expression of geranylgeranyl diphosphate synthase, and the inventive concepts may be used to facilitate the production, isolation and purification of significant quantities of recombinant geranylgeranyl diphosphate synthase (or of its primary enzyme products) for subsequent use, to obtain expression or enhanced expression of geranylgeranyl diphosphate synthase in plants, microorganisms or animals, or may be otherwise employed in an environment where the regulation or expression of geranylgeranyl diphosphate synthase is desired for the production of this synthase, or its enzyme product, or derivatives thereof. In another

aspect, the present invention relates to manipulation of the level of production of diterpenes, including paclitaxel.

Brief Description of the Drawings

The foregoing aspects and many of the attendant advantages of this invention will become more readily appreciated as the same becomes better understood by reference to the following detailed description, when taken in conjunction with the accompanying drawings, wherein:

FIGURE 1 depicts the cyclization of geranylgeranyl diphosphate to taxa-4(5),11(12)-diene and elaboration of the olefin intermediate to paclitaxel.

FIGURE 2 shows the conversion of isopentenyl diphosphate (IPP) to dimethylallyl diphosphate (DMAPP) by isopentenyl diphosphate isomerase (FIGURE 2A), and the geranylgeranyl diphosphate (GGPP) synthase-catalyzed condensation of IPP with the allylic diphosphate co-substrates DMAPP, geranyl diphosphate (GPP) and farnesyl diphosphate (FPP) (Figure 2B). The product chain-length and double bond geometry are determined by the specificity of the prenyltransferase. The solvolysis products geranylgeraniol (GGOH), geranyllinalool (GLOH) and geranylnerol (GNOH) derived by treatment of GGPP with methanolic HCl are also illustrated (FIGURE 2C).

FIGURE 3 shows the relationship of eight plant-derived GGPP synthase sequences based on amino acid similarity, as described in Example 1. Species abbreviations and Genbank accession numbers are: Arth, *Arabidopsis thaliana*, Z99708; Arth2, *A. thaliana* sequence 2, D85029 (Zhu, X.F., Suzuki, K., Okada, K., Tanaka, K., Nakagawa, T., Kawamukai, M. and Matsuda, H. (1997) *Plant Cell Physiol.*, **38**:357-361); Arth3, *A. thaliana* sequence 3, L40577 (Scolnik, P.A. and Bartley, G.E. (1995) *Plant Physiol.*, **108**:1343.); Caan, *Capsicum annuum*, X80267, (Kuntz, M., Römer, S., Suire, C., Hugueney, P., Weil, J.H., Schantz, R. and Camara, B. (1992) *Plant J.*, **2**:25-34); Caro, *Catharanthus roseus*, X92893 (Bantignies, B., Liboz, T. and Ambid, C. (1996) *Plant Physiol.*, **110**:336); Lual, *Lupinus albus*, U15778 (Aitken, S.M., Attucci, S., Ibrahim, R.K. and Gulick, P.J. (1995) *Plant Physiol.*, **108**:837-838); Sial, *Sinapis alba*, X98795 (Bonk, M., Hoffman, B., Von Lintig, J., Schledz, M., Al-Babili, S., Hobeika, E., Kleinig, H. and Beyer, P. (1997) *Eur. J. Biochem.*, **247**:942-950.); and Taca, *Taxus canadensis*, as reported herein.

FIGURE 4 shows a radio-GC analysis of the reaction product generated by *T. canadensis* GGPP synthase construct Tr²⁹⁵ followed by acid-catalyzed solvolysis as described in Example 4. The smooth lower tracing indicates the elution pattern of the

authentic standards geranylinalool (mixed isomers, the all-*trans*-isomer elutes at 20.93 min) and geranylgeraniol (R_t = 27.68 min). The radioactive component with R_t = 25.93 min is consistent with the elution behavior of geranylnerol.

FIGURE 5 shows the time course of GGPP synthase (the line marked with triangles) and taxadiene synthase (the line marked with diamonds) activity measured in extracts of *T. canadensis* suspension cell cultures following induction with methyl jasmonate, as described in Example 5. The 0 h time point corresponds to the enzyme activities from cells harvested immediately prior to methyl jasmonate addition.

Detailed Description of the Preferred Embodiment

As used herein, the terms "amino acid" and "amino acids" refer to all naturally occurring L- α -amino acids or their residues. The amino acids are identified by either the single-letter or three-letter designations:

	Asp	D	aspartic acid	Ile	I	isoleucine
	Thr	T	threonine	Leu	L	leucine
15	Ser	S	serine	Tyr	Y	tyrosine
	Glu	E	glutamic acid	Phe	F	phenylalanine
	Pro	P	proline	His	H	histidine
	Gly	G	glycine	Lys	K	lysine
	Ala	A	alanine	Arg	R	arginine
20	Cys	C	cysteine	Trp	W	tryptophan
	Val	V	valine	Gln	Q	glutamine
	Met	M	methionine	Asn	N	asparagine

As used herein, the term "nucleotide" means a monomeric unit of DNA or RNA containing a sugar moiety (pentose), a phosphate and a nitrogenous heterocyclic base. The base is linked to the sugar moiety via the glycosidic carbon (1' carbon of pentose) and that combination of base and sugar is called a nucleoside. The base characterizes the nucleotide with the four bases of DNA being adenine ("A"), guanine ("G"), cytosine ("C") and thymine ("T"). Inosine ("I") is a synthetic base that can be used to substitute for any of the four, naturally-occurring bases (A, C, G or T). The four RNA bases are A, G, C and uracil ("U"). The nucleotide sequences described herein comprise a linear array of nucleotides connected by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

"Oligonucleotide" refers to short length single or double stranded sequences of deoxyribonucleotides linked via phosphodiester bonds. The oligonucleotides are

chemically synthesized by known methods and purified, for example, on polyacrylamide gels.

The term "geranylgeranyl diphosphate synthase" (abbreviated as "GGPP synthase") is used herein to mean an enzyme capable of forming geranylgeranyl diphosphate (GGPP) by any one of, or all of, the following, numbered chemical reactions: (1) condensation of isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP) to form geranyl diphosphate (GPP), followed by condensation of GPP and IPP to form farnesyl diphosphate (FPP), followed by condensation of FPP and IPP to form GGPP; (2) condensation of GPP and IPP to form FPP, followed by condensation of FPP and IPP to form GGPP; (3) condensation of FPP and IPP to form geranylgeranyl diphosphate (GGPP).

Abbreviations used are: bp, base pair; DMAPP, dimethylallyl diphosphate; IPP, isopentenyl diphosphate; GPP, geranyl diphosphate; FPP, farnesyl diphosphate; GGPP, geranylgeranyl diphosphate; Mopso, 3-(*N*-morpholino)-2-hydroxypropane-sulfonic acid; Tris, Tris-(hydroxymethyl)aminomethane; UTR, untranslated region; TLC, thin layer chromatography; Tr, truncation site; GC, gas chromatography; Hepes, *N*-2-hydroxyethylpiperazine-*N'*-2-ethanesulfonic acid; kb, kilobase pairs.

The abbreviation "SSC" refers to a buffer used in nucleic acid hybridization solutions. One liter of the 20X (twenty times concentrate) stock SSC buffer solution (pH 7.0) contains 175.3 g sodium chloride and 88.2 g sodium citrate.

The terms "alteration", "amino acid sequence alteration", "variant" and "amino acid sequence variant" refer to geranylgeranyl diphosphate synthase molecules with some differences in their amino acid sequences as compared to the corresponding, native, i.e., naturally-occurring, geranylgeranyl diphosphate synthases. Ordinarily, the variants will possess at least about 70% homology with the corresponding native geranylgeranyl diphosphate synthases, and preferably, they will be at least about 80% homologous with the corresponding, native geranylgeranyl diphosphate synthases. The amino acid sequence variants of the geranylgeranyl diphosphate synthases falling within this invention possess substitutions, deletions, and/or insertions at certain positions. Sequence variants of geranylgeranyl diphosphate synthases may be used to attain desired enhanced or reduced enzymatic activity, modified regiochemistry or stereochemistry, or altered substrate utilization or product distribution.

Substitutional geranylgeranyl diphosphate synthase variants are those that have at least one amino acid residue in the native geranylgeranyl diphosphate synthase sequence removed and a different amino acid inserted in its place at the same position.

The substitutions may be single, where only one amino acid in the molecule has been substituted, or they may be multiple, where two or more amino acids have been substituted in the same molecule. Substantial changes in the activity of the geranylgeranyl diphosphate synthase molecules of the present invention may be
5 obtained by substituting an amino acid with a side chain that is significantly different in charge and/or structure from that of the native amino acid. This type of substitution would be expected to affect the structure of the polypeptide backbone and/or the charge or hydrophobicity of the molecule in the area of the substitution.

Moderate changes in the activity of the geranylgeranyl diphosphate synthase
10 molecules of the present invention would be expected by substituting an amino acid with a side chain that is similar in charge and/or structure to that of the native molecule. This type of substitution, referred to as a conservative substitution, would not be expected to substantially alter either the structure of the polypeptide backbone or the charge or hydrophobicity of the molecule in the area of the substitution.

Insertional geranylgeranyl diphosphate synthase variants are those with one or
15 more amino acids inserted immediately adjacent to an amino acid at a particular position in the native geranylgeranyl diphosphate synthase molecule. Immediately adjacent to an amino acid means connected to either the α -carboxy or α -amino functional group of the amino acid. The insertion may be one or more amino acids.
20 Ordinarily, the insertion will consist of one or two conservative amino acids. Amino acids similar in charge and/or structure to the amino acids adjacent to the site of insertion are defined as conservative. Alternatively, this invention includes insertion of an amino acid with a charge and/or structure that is substantially different from the amino acids adjacent to the site of insertion.

25 Deletional variants are those where one or more amino acids in the native geranylgeranyl diphosphate synthase molecules have been removed. Ordinarily, deletional variants will have one or two amino acids deleted in a particular region of the geranylgeranyl diphosphate synthase molecule.

The terms "biological activity", "biologically active", "activity" and "active"
30 refer to the ability of the geranylgeranyl diphosphate synthases of the present invention to catalyze the formation of geranylgeranyl diphosphate (GGPP) by any one of, or all of, the following chemical reactions and sequence of chemical reactions: (1) condensation of isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP) to form geranyl diphosphate (GPP), followed by condensation of GPP and
35 IPP to form farnesyl diphosphate (FPP), followed by condensation of FPP and IPP to

form GGPP; (2) condensation of GPP and IPP to form FPP, followed by condensation of FPP and IPP to form GGPP; (3) condensation of FPP and IPP to form geranylgeranyl diphosphate (GGPP). Geranylgeranyl diphosphate synthase activity is measured in an enzyme activity assay, such as the assay described in
5 Example 4. Amino acid sequence variants of the geranylgeranyl diphosphate synthases of the present invention may have desirable altered biological activity including, for example, altered reaction kinetics, substrate utilization, product distribution or other characteristics such as regiochemistry and stereochemistry.

The terms "DNA sequence encoding", "DNA encoding" "nucleic acid
10 molecule encoding" and "nucleic acid encoding" refer to the order or sequence of deoxyribonucleotides along a strand of deoxyribonucleic acid. The order of these deoxyribonucleotides determines the order of amino acids along the translated polypeptide chain. The DNA sequence thus codes for the amino acid sequence.

The terms "replicable vector" "replicable expression vector" and "expression
15 vector" refer to a piece of DNA, usually double-stranded, which may have inserted into it another piece of DNA (the insert DNA) such as, but not limited to, a cDNA molecule. The vector is used to transport the insert DNA into a suitable host cell. The insert DNA may be derived from the host cell, or may be derived from a different cell or organism. Once in the host cell, the vector can replicate independently of or
20 coincidental with the host chromosomal DNA, and several copies of the vector and its inserted DNA may be generated. The terms "replicable expression vector" and "expression vector" refer exclusively to vectors that contain the necessary elements that permit translating the insert DNA into a polypeptide. Many molecules of the polypeptide encoded by the insert DNA can thus be rapidly synthesized.

25 The terms "transformed host cell," "transformed" and "transformation" refer to the introduction of DNA into a cell. The cell is termed a "host cell", and it may be a prokaryotic or a eukaryotic cell. Typical prokaryotic host cells include various strains of *E. coli*. Typical eukaryotic host cells are plant cells, such as maize cells, yeast cells, insect cells or animal cells. The introduced DNA is usually in the form of a
30 vector containing an inserted piece of DNA. The introduced DNA sequence may be from the same species as the host cell or from a different species from the host cell, or it may be a hybrid DNA sequence, containing some foreign DNA and some DNA derived from the host species.

In accordance with the present invention, a cDNA (SEQ ID NO:1) encoding
35 geranylgeranyl diphosphate synthase (SEQ ID NO:2) from Canadian Yew (*Taxus*

canadensis) was isolated and sequenced in the following manner. A phage cDNA library from induced *T. canadensis* cells was prepared in λ PG15. Total RNA was isolated from 14-day-old suspension cell cultures which had been induced with 200 μ M methyl jasmonate 7 d prior to harvest by filtration. PolyA⁺ RNA was prepared by chromatography on oligo(dT)-cellulose.

An initial PCR product was amplified using 150 pmol/reaction of a reverse degenerate primer (SEQ ID NO:3), which corresponded to part of a specific amino acid sequence which was conserved among certain acetyltransferase enzymes. This primer fortuitously hybridized to two different regions of a geranylgeranyl diphosphate synthase mRNA. The resulting 861 bp fragment was ligated into pCR 2.1 Topo and the recombinant vector was transformed into *E. coli* XL1-Blue cells. Forty-five positive colonies were isolated from which plasmids were purified then sequenced. Only one isolated plasmid contained an insert sequence (SEQ ID NO:4) resembling geranylgeranyl diphosphate synthases from angiosperm plant species. When compared to other GGPP synthase sequences, this clone (SEQ ID NO:4) was found to encode the first 194 amino acids of the translated protein in addition to 279 bp of the 5'-UTR.

A 583 bp portion of this initial PCR product (extending from nucleotide 279 to nucleotide 861 of the 861 bp cDNA sequence set forth in SEQ ID NO:4) was used as a hybridization probe to obtain a full-length geranylgeranyl diphosphate synthase cDNA sequence. Thus, a nondegenerate forward primer (SEQ ID NO:5) and a nondegenerate reverse primer (SEQ ID NO:6) were designed which corresponded to nucleotides 279 to 300, and 839 to 861, respectively, of the 861 bp cDNA sequence set forth in SEQ ID NO:4. Nondegenerate forward primer (SEQ ID NO:5) and nondegenerate reverse primer (SEQ ID NO:6) were used to amplify the intervening 583 bp region of the 861 bp cDNA sequence set forth in SEQ ID NO:4.

The resulting, gel purified, amplified, cDNA fragment was then labeled with [α -³²P]ATP and used to probe the *T. canadensis* cDNA library, containing approximately 80,000 independent clones. Sixteen positive clones were obtained, of which five encoded a putative geranylgeranyl diphosphate synthase protein.

The sequence of four of the five putative geranylgeranyl diphosphate synthase cDNA clones was identical and is set forth in SEQ ID NO:1. One full-length coding region, free of stop codons, was identified which begins 308 bp from the 5'-terminus of the sequence set forth in SEQ ID NO:1, and ends at a UGA codon at position 1489

of the sequence set forth in SEQ ID NO:1, thereby yielding a coding region of 1182 bp, with a 5'-UTR of 308 bp and a 3'-UTR of approximately 400 bp.

All known GGPP synthase sequences of plant origin appear to encode a transit peptide for organellar compartmentation of this prenyltransferase. Many of these enzymes have been shown to be localized to plastids. Since it was assumed that the *T. canadensis* GGPP synthase cDNA likewise would encode an organellar transit peptide, and that the resulting preprotein would likely be less catalytically efficient than the mature, proteolytically processed form, the deduced amino acid sequence of the putative, *Taxus* GGPP synthase (SEQ ID NO:2) was compared to angiosperm GGPP synthase sequences in order to identify the N-terminal and C-terminal boundaries of the mature protein.

Thus, comparison of plant-derived GGPP synthase amino acid sequences with the deduced *T. canadensis* protein (SEQ ID NO:2) showed that high-level conservation begins at F⁹⁹ of the amino acid sequence set forth in SEQ ID NO:2, indicating a logical truncation site at nucleotide 295 (Tr²⁹⁵) of the GGPP synthase cDNA sequence set forth in SEQ ID NO:1; a second site (at nucleotide 313, Tr³¹³) was chosen (six residues downstream) because of the location of the convenient M¹⁰⁵ residue.

PCR primers containing a *Kpn*I site (SEQ ID NO:7) or a *Bam*HI site (SEQ ID NO:8) were designed to the 3'- and 5'-termini, respectively, of the presumptive full-length coding sequence. Additionally, a 5'-terminal primer (SEQ ID NO:9) (containing a *Bam*HI site) was designed to generate a 5'-truncated version of the GGPP synthase protein sequence set forth in SEQ ID NO:2 beginning at Tr²⁹⁵, while a second 5'-terminal primer (SEQ ID NO:10) (containing a *Bam*HI site) was designed to generate a 5'-truncated version of the GGPP synthase protein sequence set forth in SEQ ID NO:2 beginning at Tr³¹³. Thus, the 5'-truncated versions of the GGPP synthase protein generated by the primer combinations SEQ ID NO:9 plus SEQ ID NO:7, and SEQ ID NO:10 plus SEQ ID NO:7 both lacked a transit peptide. After amplification with *Pfu* DNA polymerase, the *Bam*HI/*Kpn*I-digested fragment corresponding to each coding sequence was then subcloned into pYeDP60.

The three pYeDP60/*T. canadensis* GGPP synthase constructs were transformed and expressed in ANY119, an *S. cerevisiae* mutant (the bet2-1 mutant) that is defective for the β -subunit of type II geranylgeranyltransferase. This mutation is lethal at high temperature but can be complemented by increasing the expression level of GGPP synthase. To determine if the three *T. canadensis* GGPP synthase

forms (the full-length preprotein, the 5'-truncated protein beginning at Tr²⁹⁵ and the 5'-truncated protein beginning at Tr³¹³) could be functionally expressed in yeast at levels sufficient to rescue this mutant when grown at the restrictive temperature, the expression of the three constructs was tested on three different carbon sources that differentially regulate GAL10-CYC1 promoter activity. The results of these expression studies indicated that both the full-length GGPP synthase clone (SEQ ID NO:1) and the Tr²⁹⁵ truncation rescue the *bet2-1* mutant and that, even under repressed conditions, enough leaky expression of GGPP synthase occurs to complement the mutation. When high level expression of the heterologous GGPP synthase was fully induced in yeast, the gene was toxic to the host yeast cells. The expression studies in yeast demonstrated that the full-length and Tr²⁹⁵ GGPP synthase constructs yield active GGPP synthase, but the shorter Tr³¹³ truncation construct does not.

Additionally, a phage cDNA library from induced *T. cuspidata* cells was prepared in λPG15. Total RNA was isolated using an RNA Maxi kit (Qiagen) from 14-day-old suspension cell cultures which had been induced with 200 μM methyl jasmonate 7 d prior to harvest by filtration. PolyA⁺ RNA was prepared by chromatography on oligo(dT)-cellulose (Pharmacia Biotech). The cDNA library was synthesized using a λZAP-cDNA synthesis kit and ZAP-cDNA gigapack III gold cloning kit (Stratagene) by following the manufacturer's instructions, except that λPG15 replaced λZAP as the cloning vector.

A partial-length cDNA clone (SEQ ID NO:11) encoding a GGPP synthase (SEQ ID NO:12) was amplified by PCR using the primers set forth in SEQ ID NO:7 and SEQ ID NO:9. The *T. cuspidata* GGPP synthase partial cDNA (SEQ ID NO:11) encodes the mature form of the *T. cuspidata* GGPP synthase enzyme, *i.e.*, the form of the enzyme that lacks the transit peptide at the amino terminus. The deduced amino acid sequence of the *T. cuspidata* enzyme (SEQ ID NO:12) is identical to the mature form of the *T. canadensis* enzyme. At the nucleotide level, the *T. cuspidata* cDNA (SEQ ID NO:11) is almost identical (98.6% similarity) to the *T. canadensis* GGPP synthase cDNA (SEQ ID NO:1).

The isolation of cDNAs (SEQ ID NO:1; SEQ ID NO:11) encoding geranylgeranyl diphosphate synthase (SEQ ID NO:2; SEQ ID NO:12) permits the development of efficient expression systems for this functional enzyme; provides useful tools for examining the developmental regulation of GGPP synthase; permits investigation of the reaction mechanism(s) of this enzyme, and permits the isolation of

other geranylgeranyl diphosphate synthases. For example, the nucleic acids of the present invention can be used as hybridization probes to identify geranylgeranyl diphosphate synthase genes from microorganisms, such as *Taxomyces andreanae* and *Penicillium raistrickii*, that are capable of producing paclitaxel. The isolation of
5 geranylgeranyl diphosphate synthase cDNAs (SEQ ID NO:1; SEQ ID NO:11) also permits the transformation of a wide range of organisms in order to enhance, or otherwise alter, the synthesis of geranylgeranyl diphosphate, and of its derivative diterpenes, such as paclitaxel.

Although the geranylgeranyl diphosphate synthase protein set forth in SEQ ID
10 NO:2 directs the enzyme to plastids, substitution of the presumptive targeting sequence of this enzyme (SEQ ID NO:2, amino acid residue numbers 1 to 98) with other transport sequences well known in the art (See, for example, the following publications, the cited portions of which are incorporated by reference herein: von Heijne et al., *Eur. J. Biochem.*, **180**:535-545, 1989; Stryer, *Biochemistry*,
15 W.H. Freeman and Company, New York, NY, p. 769 [1988]) may be employed to direct geranylgeranyl diphosphate synthase to other cellular or extracellular locations.

In addition to the native geranylgeranyl diphosphate synthase amino acid sequence of, for example, SEQ ID NO:2, sequence variants produced by deletions, substitutions, mutations and/or insertions are intended to be within the scope of the
20 invention except insofar as limited by the prior art. The geranylgeranyl diphosphate synthase amino acid sequence variants of this invention may be constructed by mutating the DNA sequences that encode the wild-type synthases, such as by using techniques commonly referred to as site-directed mutagenesis. Nucleic acid molecules encoding the geranylgeranyl diphosphate synthases of the present invention
25 can be mutated by a variety of PCR techniques well known to one of ordinary skill in the art. (See, for example, the following publications, the cited portions of which are incorporated by reference herein: "PCR Strategies", M.A. Innis, D.H. Gelfand and J.J. Sninsky, eds., 1995, Academic Press, San Diego, CA (Chapter 14); "PCR Protocols: A Guide to Methods and Applications", M.A. Innis, D.H. Gelfand, J.J.
30 Sninsky and T.J. White, eds., Academic Press, NY (1990).

By way of non-limiting example, the two primer system utilized in the Transformer Site-Directed Mutagenesis kit from Clontech, may be employed for introducing site-directed mutants into the geranylgeranyl diphosphate synthase genes of the present invention. Following denaturation of the target plasmid in this system,
35 two primers are simultaneously annealed to the plasmid; one of these primers contains

the desired site-directed mutation, the other contains a mutation at another point in the plasmid resulting in elimination of a restriction site. Second strand synthesis is then carried out, tightly linking these two mutations, and the resulting plasmids are transformed into a *mutS* strain of *E. coli*. Plasmid DNA is isolated from the transformed bacteria, restricted with the relevant restriction enzyme (thereby linearizing the unmutated plasmids), and then retransformed into *E. coli*. This system allows for generation of mutations directly in an expression plasmid, without the necessity of subcloning or generation of single-stranded phagemids. The tight linkage of the two mutations and the subsequent linearization of unmutated plasmids results in high mutation efficiency and allows minimal screening. Following synthesis of the initial restriction site primer, this method requires the use of only one new primer type per mutation site. Rather than prepare each positional mutant separately, a set of "designed degenerate" oligonucleotide primers can be synthesized in order to introduce all of the desired mutations at a given site simultaneously. Transformants can be screened by sequencing the plasmid DNA through the mutagenized region to identify and sort mutant clones. Each mutant DNA can then be fully sequenced or restricted and analyzed by electrophoresis on Mutation Detection Enhancement gel (J.T. Baker) to confirm that no other alterations in the sequence have occurred (by band shift comparison to the unmutagenized control).

Again, by way of non-limiting example, the two primer system utilized in the QuikChange™ Site-Directed Mutagenesis kit from Stratagene (LaJolla, California), may be employed for introducing site-directed mutants into the geranylgeranyl diphosphate synthase genes of the present invention. Double-stranded plasmid DNA, containing the insert bearing the target mutation site, is denatured and mixed with two oligonucleotides complementary to each of the strands of the plasmid DNA at the target mutation site. The annealed oligonucleotide primers are extended using *Pfu* DNA polymerase, thereby generating a mutated plasmid containing staggered nicks. After temperature cycling, the unmutated, parental DNA template is digested with restriction enzyme *DpnI* which cleaves methylated or hemimethylated DNA, but which does not cleave unmethylated DNA. The parental, template DNA is almost always methylated or hemimethylated since most strains of *E. coli*, from which the template DNA is obtained, contain the required methylase activity. The remaining, annealed vector DNA incorporating the desired mutation(s) is transformed into *E. coli*.

The mutated geranylgeranyl diphosphate synthase gene can be cloned into a pET (or other) overexpression vector that can be employed to transform *E. coli* such as strain *E. coli* BL21(DE3)pLysS, for high level production of the mutant protein, and purification by standard protocols. Examples of plasmid vectors and *E. coli* strains that can be used to express high levels of the geranylgeranyl diphosphate synthase proteins of the present invention are set forth in Sambrook et al, *Molecular Cloning, A Laboratory Manual*, 2nd Edition (1989), Chapter 17. The method of FAB-MS mapping can be employed to rapidly check the fidelity of mutant expression. This technique provides for sequencing segments throughout the whole protein and provides the necessary confidence in the sequence assignment. In a mapping experiment of this type, protein is digested with a protease (the choice will depend on the specific region to be modified since this segment is of prime interest and the remaining map should be identical to the map of unmutagenized protein). The set of cleavage fragments is fractionated by microbore HPLC (reversed phase or ion exchange, again depending on the specific region to be modified) to provide several peptides in each fraction, and the molecular weights of the peptides are determined by FAB-MS. The masses are then compared to the molecular weights of peptides expected from the digestion of the predicted sequence, and the correctness of the sequence quickly ascertained. Since the exemplary mutagenesis techniques set forth herein produce site-directed mutations, sequencing of the altered peptide should not be necessary if the mass spectrograph agrees with prediction. If necessary to verify a changed residue, CAD-tandem MS/MS can be employed to sequence the peptides of the mixture in question, or the target peptide can be purified for subtractive Edman degradation or carboxypeptidase Y digestion depending on the location of the modification.

In the design of a particular site directed mutagenesis experiment, it is generally desirable to first make a non-conservative substitution (e.g., Ala for Cys, His or Glu) and determine if activity is greatly impaired as a consequence. The properties of the mutagenized protein are then examined with particular attention to the kinetic parameters of K_m and k_{cat} as sensitive indicators of altered function, from which changes in binding and/or catalysis *per se* may be deduced by comparison to the native enzyme. If the residue is by this means demonstrated to be important by activity impairment, or knockout, then conservative substitutions can be made, such as Asp for Glu to alter side chain length, Ser for Cys, or Arg for His. For hydrophobic segments, it is largely size that is usefully altered, although aromatics can

also be substituted for alkyl side chains. Changes in the normal product distribution can indicate which step(s) of the reaction sequence have been altered by the mutation. Modification of the hydrophobic pocket can be employed to change binding conformations for substrates and result in altered regiochemistry and/or stereochemistry.

Other site directed mutagenesis techniques may also be employed with the nucleotide sequences of the invention. For example, restriction endonuclease digestion of DNA followed by ligation may be used to generate deletion variants of geranylgeranyl diphosphate synthase, as described in section 15.3 of Sambrook et al. *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, New York, NY [1989], incorporated herein by reference. A similar strategy may be used to construct insertion variants, as described in section 15.3 of Sambrook et al., *supra*.

Oligonucleotide-directed mutagenesis may also be employed for preparing substitution variants of this invention. It may also be used to conveniently prepare the deletion and insertion variants of this invention. This technique is well known in the art as described by Adelman et al. (*DNA* 2:183 [1983]); Sambrook et al., *supra*; "Current Protocols in Molecular Biology", 1991, Wiley (NY), F.T. Ausubel, R. Brent, R.E. Kingston, D.D. Moore, J.D. Seidman, J.A. Smith and K. Struhl, eds, incorporated herein by reference.

Generally, oligonucleotides of at least 25 nucleotides in length are used to insert, delete or substitute two or more nucleotides in the geranylgeranyl diphosphate synthase molecule. An optimal oligonucleotide will have 12 to 15 perfectly matched nucleotides on either side of the nucleotides coding for the mutation. To mutagenize wild-type geranylgeranyl diphosphate synthase, the oligonucleotide is annealed to the single-stranded DNA template molecule under suitable hybridization conditions. A DNA polymerizing enzyme, usually the Klenow fragment of *E. coli* DNA polymerase I, is then added. This enzyme uses the oligonucleotide as a primer to complete the synthesis of the mutation-bearing strand of DNA. Thus, a heteroduplex molecule is formed such that one strand of DNA encodes the wild-type synthase inserted in the vector, and the second strand of DNA encodes the mutated form of the synthase inserted into the same vector. This heteroduplex molecule is then transformed into a suitable host cell.

Mutants with more than one amino acid substituted may be generated in one of several ways. If the amino acids are located close together in the polypeptide

chain, they may be mutated simultaneously using one oligonucleotide that codes for all of the desired amino acid substitutions. If, however, the amino acids are located some distance from each other (separated by more than ten amino acids, for example) it is more difficult to generate a single oligonucleotide that encodes all of the desired changes. Instead, one of two alternative methods may be employed. In the first method, a separate oligonucleotide is generated for each amino acid to be substituted. The oligonucleotides are then annealed to the single-stranded template DNA simultaneously, and the second strand of DNA that is synthesized from the template will encode all of the desired amino acid substitutions. An alternative method involves two or more rounds of mutagenesis to produce the desired mutant. The first round is as described for the single mutants: wild-type geranylgeranyl diphosphate synthase DNA is used for the template, an oligonucleotide encoding the first desired amino acid substitution(s) is annealed to this template, and the heteroduplex DNA molecule is then generated. The second round of mutagenesis utilizes the mutated DNA produced in the first round of mutagenesis as the template. Thus, this template already contains one or more mutations. The oligonucleotide encoding the additional desired amino acid substitution(s) is then annealed to this template, and the resulting strand of DNA now encodes mutations from both the first and second rounds of mutagenesis. This resultant DNA can be used as a template in a third round of mutagenesis, and so on.

A gene encoding geranylgeranyl diphosphate synthase may be incorporated into any organism (intact plant, animal, microbe, etc.), or cell culture derived therefrom, that produces substrates that can be converted to geranylgeranyl diphosphate. A geranylgeranyl diphosphate synthase gene may be introduced into any organism for a variety of purposes including, but not limited to: production of geranylgeranyl diphosphate synthase, or its product geranylgeranyl diphosphate; enhancement of the rate of production and/or the absolute amount of one or more diterpenes derived from geranylgeranyl diphosphate; enhancement of the rate of production and/or the absolute amount of paclitaxel or related taxoids; the enhanced production of resin acids; the enhanced production of gibberellin plant hormones. While the nucleic acid molecules of the present invention can be introduced into any organism, the nucleic acid molecules of the present invention will preferably be introduced into a gymnosperm species, most preferably a *Taxus* species.

Advantages associated with expression of the nucleic acid molecules of the present invention in a gymnosperm species, most preferably a *Taxus* species, include,

but are not limited to: (1) compatible codon usage for maximum translational efficiency; (2) recognition of the encoded preprotein by the plastid import system; (3) maximum fidelity in proteolytic processing by the plastids to the mature enzyme form and (4) optimum protein-protein interaction with upstream and downstream enzymes of the paclitaxel pathway for most efficient channeling of metabolites.

Eukaryotic expression systems may be utilized for the production of geranylgeranyl diphosphate synthase since they are capable of carrying out any required posttranslational modifications and of directing the enzyme to the proper cellular compartment. A representative eukaryotic expression system for this purpose uses the recombinant baculovirus, *Autographa californica* nuclear polyhedrosis virus (AcNPV; M.D. Summers and G.E. Smith, *A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures* [1986]; Luckow et al., *Bio-technology*, 6:47-55 [1987]) for expression of the geranylgeranyl diphosphate synthases of the invention. Infection of insect cells (such as cells of the species *Spodoptera frugiperda*) with the recombinant baculoviruses allows for the production of large amounts of the geranylgeranyl diphosphate synthase proteins. In addition, the baculovirus system has other important advantages for the production of recombinant geranylgeranyl diphosphate synthase. For example, baculoviruses do not infect humans and can therefore be safely handled in large quantities. In the baculovirus system, a DNA construct is prepared including a DNA segment encoding geranylgeranyl diphosphate synthase and a vector. The vector may comprise the polyhedron gene promoter region of a baculovirus, the baculovirus flanking sequences necessary for proper cross-over during recombination (the flanking sequences comprise about 200-300 base pairs adjacent to the promoter sequence) and a bacterial origin of replication which permits the construct to replicate in bacteria. The vector is constructed so that (i) the DNA segment is placed adjacent (or operably linked or "downstream" or "under the control of") to the polyhedron gene promoter and (ii) the promoter/geranylgeranyl diphosphate synthase combination is flanked on both sides by 200-300 base pairs of baculovirus DNA (the flanking sequences).

To produce the geranylgeranyl diphosphate synthase DNA construct, a cDNA clone encoding the full length geranylgeranyl diphosphate synthase is obtained using methods such as those described herein. The DNA construct is contacted in a host cell with baculovirus DNA of an appropriate baculovirus (that is, of the same species of baculovirus as the promoter encoded in the construct) under conditions such that recombination is effected. The resulting recombinant baculoviruses encode the full

geranylgeranyl diphosphate synthase. For example, an insect host cell can be cotransfected or transfected separately with the DNA construct and a functional baculovirus. Resulting recombinant baculoviruses can then be isolated and used to infect cells to effect production of the geranylgeranyl diphosphate synthase. Host insect cells include, for example, *Spodoptera frugiperda* cells, that are capable of producing a baculovirus-expressed geranylgeranyl diphosphate synthase. Insect host cells infected with a recombinant baculovirus of the present invention are then cultured under conditions allowing expression of the baculovirus-encoded geranylgeranyl diphosphate synthase. Geranylgeranyl diphosphate synthase thus produced is then extracted from the cells using methods known in the art.

Other eukaryotic microbes such as yeasts may also be used to practice this invention. The baker's yeast *Saccharomyces cerevisiae*, is a commonly used yeast, although several other strains are available. The plasmid YRp7 (Stinchcomb et al., *Nature*, **282**:39 [1979]; Kingsman et al., *Gene* **7**:141 [1979]; Tschemper et al., *Gene*, **10**:157 [1980]) is commonly used as an expression vector in *Saccharomyces*. This plasmid contains the *trp1* gene that provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, such as strains ATCC No. 44,076 and PEP4-1 (Jones, *Genetics*, **85**:12 [1977]). The presence of the *trp1* lesion as a characteristic of the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan. Yeast host cells are generally transformed using the polyethylene glycol method, as described by Hinnen (*Proc. Natl. Acad. Sci. USA*, **75**:1929 [1978]). Additional yeast transformation protocols are set forth in Gietz et al., *N.A.R.*, **20**(17):1425(1992); Reeves et al., *FEMS*, **99**(2-3):193-197, (1992), both of which publications are incorporated herein by reference.

Suitable promoting sequences in yeast vectors include the promoters for 3-phosphoglycerate kinase (Hitzeman et al., *J. Biol. Chem.*, **255**:2073 [1980]) or other glycolytic enzymes (Hess et al., *J. Adv. Enzyme Reg.* **7**:149 [1968]; Holland et al., *Biochemistry*, **17**:4900 [1978]), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. In the construction of suitable expression plasmids, the termination sequences associated with these genes are also ligated into the expression vector 3' of the sequence desired to be expressed to provide polyadenylation of the mRNA and termination. Other

promoters that have the additional advantage of transcription controlled by growth conditions are the promoter region for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, and the aforementioned glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Any plasmid vector containing yeast-compatible promoter, origin of replication and termination sequences is suitable.

Cell cultures derived from multicellular organisms, such as plants, may be used as hosts to practice this invention. Transgenic plants can be obtained, for example, by transferring plasmids that encode geranylgeranyl diphosphate synthase and a selectable marker gene, *e.g.*, the kan gene encoding resistance to kanamycin, into *Agrobacterium tumefaciens* containing a helper Ti plasmid as described in Hoeckema et al., *Nature*, **303**:179-181 [1983] and culturing the *Agrobacterium* cells with leaf slices, or other tissues or cells, of the plant to be transformed as described by An et al., *Plant Physiology*, **81**:301-305 [1986]. Transformation of cultured plant host cells is normally accomplished through *Agrobacterium tumefaciens*. Cultures of mammalian host cells and other host cells that do not have rigid cell membrane barriers are usually transformed using the calcium phosphate method as originally described by Graham and Van der Eb (*Virology*, **52**:546 [1978]) and modified as described in sections 16.32-16.37 of Sambrook et al., *supra*. However, other methods for introducing DNA into cells such as Polybrene (Kawai and Nishizawa, *Mol. Cell. Biol.*, **4**:1172 [1984]), protoplast fusion (Schaffner, *Proc. Natl. Acad. Sci. USA*, **77**:2163 [1980]), electroporation (Neumann et al., *EMBO J.*, **1**:841 [1982]), and direct microinjection into nuclei (Capecchi, *Cell*, **22**:479 [1980]) may also be used. Additionally, animal transformation strategies are reviewed in Monastersky G.M. and Robl, J.M., *Strategies in Transgenic Animal Science*, ASM Press, Washington, D.C., 1995, incorporated herein by reference. Transformed plant calli may be selected through the selectable marker by growing the cells on a medium containing, *e.g.*, kanamycin, and appropriate amounts of phytohormone such as naphthalene acetic acid and benzyladenine for callus and shoot induction. The plant cells may then be regenerated and the resulting plants transferred to soil using techniques well known to those skilled in the art.

In addition, a gene regulating geranylgeranyl diphosphate synthase production can be incorporated into the plant along with a necessary promoter which is inducible. In the practice of this embodiment of the invention, a promoter that only responds to a specific external or internal stimulus is fused to the target cDNA. Thus, the gene

will not be transcribed except in response to the specific stimulus. As long as the gene is not being transcribed, its gene product is not produced.

An illustrative example of a responsive promoter system that can be used in the practice of this invention is the glutathione-S-transferase (GST) system in maize. GSTs are a family of enzymes that can detoxify a number of hydrophobic electrophilic compounds that often are used as pre-emergent herbicides (Weigand et al., *Plant Molecular Biology*, 7:235-243 [1986]). Studies have shown that the GSTs are directly involved in causing this enhanced herbicide tolerance. This action is primarily mediated through a specific 1.1 kb mRNA transcription product. In short, maize has a naturally occurring quiescent gene already present that can respond to external stimuli and that can be induced to produce a gene product. This gene has previously been identified and cloned. Thus, in one embodiment of this invention, the promoter is removed from the GST responsive gene and attached to a geranylgeranyl diphosphate synthase gene that previously has had its native promoter removed. This engineered gene is the combination of a promoter that responds to an external chemical stimulus and a gene responsible for successful production of geranylgeranyl diphosphate synthase.

In addition to the methods described above, several methods are known in the art for transferring cloned DNA into a wide variety of plant species, including gymnosperms, angiosperms, monocots and dicots (see, e.g., Glick and Thompson, eds., *Methods in Plant Molecular Biology*, CRC Press, Boca Raton, Florida [1993], incorporated by reference herein). Representative examples include electroporation-facilitated DNA uptake by protoplasts in which an electrical pulse transiently permeabilizes cell membranes, permitting the uptake of a variety of biological molecules, including recombinant DNA (Rhodes et al., *Science*, 240(4849):204-207 [1988]); treatment of protoplasts with polyethylene glycol (Lyznik et al., *Plant Molecular Biology*, 13:151-161 [1989]); and bombardment of cells with DNA-laden microprojectiles which are propelled by explosive force or compressed gas to penetrate the cell wall (Klein et al., *Plant Physiol.* 91:440-444 [1989] and Boynton et al., *Science*, 240(4858):1534-1538 [1988]). Transformation of *Taxus* species can be achieved, for example, by employing the methods set forth in Han et al, *Plant Science*, 95:187-196 (1994), incorporated by reference herein. A method that has been applied to Rye plants (*Secale cereale*) is to directly inject plasmid DNA, including a selectable marker gene, into developing floral tillers (de la Pena et al., *Nature* 325:274-276 (1987)). Further, plant viruses can be used as

vectors to transfer genes to plant cells. Examples of plant viruses that can be used as vectors to transform plants include the Cauliflower Mosaic Virus (Brisson et al., *Nature* **310**: 511-514 (1984); Additionally, plant transformation strategies and techniques are reviewed in Birch, R.G., *Ann Rev Plant Phys Plant Mol Biol*, **48**:297
5 (1997); Forester et al., *Exp. Agric.*, **33**:15-33 (1997). The aforementioned publications disclosing plant transformation techniques are incorporated herein by reference, and minor variations make these technologies applicable to a broad range of plant species.

Each of these techniques has advantages and disadvantages. In each of the
10 techniques, DNA from a plasmid is genetically engineered such that it contains not only the gene of interest, but also selectable and screenable marker genes. A selectable marker gene is used to select only those cells that have integrated copies of the plasmid (the construction is such that the gene of interest and the selectable and screenable genes are transferred as a unit). The screenable gene provides another
15 check for the successful culturing of only those cells carrying the genes of interest. A commonly used selectable marker gene is neomycin phosphotransferase II (NPT II). This gene conveys resistance to kanamycin, a compound that can be added directly to the growth media on which the cells grow. Plant cells are normally susceptible to kanamycin and, as a result, die. The presence of the NPT II gene overcomes the
20 effects of the kanamycin and each cell with this gene remains viable. Another selectable marker gene which can be employed in the practice of this invention is the gene which confers resistance to the herbicide glufosinate (Basta). A screenable gene commonly used is the β -glucuronidase gene (GUS). The presence of this gene is characterized using a histochemical reaction in which a sample of putatively
25 transformed cells is treated with a GUS assay solution. After an appropriate incubation, the cells containing the GUS gene turn blue.

The plasmid containing one or more of these genes is introduced into either plant protoplasts or callus cells by any of the previously mentioned techniques. If the
30 marker gene is a selectable gene, only those cells that have incorporated the DNA package survive under selection with the appropriate phytotoxic agent. Once the appropriate cells are identified and propagated, plants are regenerated. Progeny from the transformed plants must be tested to insure that the DNA package has been successfully integrated into the plant genome.

Mammalian host cells may also be used in the practice of the invention.
35 Examples of suitable mammalian cell lines include monkey kidney CV1 line

transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line 293S (Graham et al., *J. Gen. Virol.*, **36**:59 [1977]); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells (Urlab and Chasin, *Proc. Natl. Acad. Sci USA* **77**:4216 [1980]); mouse sertoli cells (TM4, Mather, *Biol. Reprod.*, **23**:243 [1980]); monkey kidney cells (CV1-76, ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); mouse mammary tumor cells (MMT 060562, ATCC CCL 51); rat hepatoma cells (HTC, MI.54, Baumann et al., *J. Cell Biol.*, **85**:1 [1980]); and TRI cells (Mather et al., *Annals N.Y. Acad. Sci.*, **383**:44 [1982]). Expression vectors for these cells ordinarily include (if necessary) DNA sequences for an origin of replication, a promoter located in front of the gene to be expressed, a ribosome binding site, an RNA splice site, a polyadenylation site, and a transcription terminator site.

Promoters used in mammalian expression vectors are often of viral origin. These viral promoters are commonly derived from polyoma virus, Adenovirus 2, and most frequently Simian Virus 40 (SV40). The SV40 virus contains two promoters that are termed the early and late promoters. These promoters are particularly useful because they are both easily obtained from the virus as one DNA fragment that also contains the viral origin of replication (Fiers et al., *Nature*, **273**:113 [1978]). Smaller or larger SV40 DNA fragments may also be used, provided they contain the approximately 250-bp sequence extending from the HindIII site toward the BglI site located in the viral origin of replication.

Alternatively, promoters that are naturally associated with the foreign gene (homologous promoters) may be used provided that they are compatible with the host cell line selected for transformation.

An origin of replication may be obtained from an exogenous source, such as SV40 or other virus (e.g., Polyoma, Adeno, VSV, BPV) and inserted into the cloning vector. Alternatively, the origin of replication may be provided by the host cell chromosomal replication mechanism. If the vector containing the foreign gene is integrated into the host cell chromosome, the latter is often sufficient.

The use of a secondary DNA coding sequence can enhance production levels of geranylgeranyl diphosphate synthase in transformed cell lines. The secondary coding sequence typically comprises the enzyme dihydrofolate reductase (DHFR).

The wild-type form of DHFR is normally inhibited by the chemical methotrexate (MTX). The level of DHFR expression in a cell will vary depending on the amount of MTX added to the cultured host cells. An additional feature of DHFR that makes it particularly useful as a secondary sequence is that it can be used as a selection marker to identify transformed cells. Two forms of DHFR are available for use as secondary sequences, wild-type DHFR and MTX-resistant DHFR. The type of DHFR used in a particular host cell depends on whether the host cell is DHFR deficient (such that it either produces very low levels of DHFR endogenously, or it does not produce functional DHFR at all). DHFR-deficient cell lines such as the CHO cell line described by Urlaub and Chasin, *supra*, are transformed with wild-type DHFR coding sequences. After transformation, these DHFR-deficient cell lines express functional DHFR and are capable of growing in a culture medium lacking the nutrients hypoxanthine, glycine and thymidine. Nontransformed cells will not survive in this medium.

The MTX-resistant form of DHFR can be used as a means of selecting for transformed host cells in those host cells that endogenously produce normal amounts of functional DHFR that is MTX sensitive. The CHO-K1 cell line (ATCC No. CL 61) possesses these characteristics, and is thus a useful cell line for this purpose. The addition of MTX to the cell culture medium will permit only those cells transformed with the DNA encoding the MTX-resistant DHFR to grow. The nontransformed cells will be unable to survive in this medium.

Prokaryotes may also be used as host cells for the initial cloning steps of this invention. They are particularly useful for rapid production of large amounts of DNA, for production of single-stranded DNA templates used for site-directed mutagenesis, for screening many mutants simultaneously, and for DNA sequencing of the mutants generated. Suitable prokaryotic host cells include *E. coli* K12 strain 94 (ATCC No. 31,446), *E. coli* strain W3110 (ATCC No. 27,325) *E. coli* X1776 (ATCC No. 31,537), and *E. coli* B; however many other strains of *E. coli*, such as HB101, JM101, NM522, NM538, NM539, and many other species and genera of prokaryotes including bacilli such as *Bacillus subtilis*, other enterobacteriaceae such as *Salmonella typhimurium* or *Serratia marcesans*, and various *Pseudomonas* species may all be used as hosts. Prokaryotic host cells or other host cells with rigid cell walls are preferably transformed using the calcium chloride method as described in section 1.82 of Sambrook et al., *supra*. Alternatively, electroporation may be used for transformation of these cells. Prokaryote transformation techniques are set forth in

Dower, W.J., in *Genetic Engineering, Principles and Methods*, 12:275-296, Plenum Publishing Corp., 1990; Hanahan et al., *Meth. Enzymol.*, 204:63 (1991).

As a representative example, cDNA sequences encoding geranylgeranyl diphosphate synthase may be transferred to the (His)₆-Tag pET vector commercially available (from Novagen) for overexpression in *E. coli* as heterologous host. This pET expression plasmid has several advantages in high level heterologous expression systems. The desired cDNA insert is ligated in frame to plasmid vector sequences encoding six histidines followed by a highly specific protease recognition site (thrombin) that are joined to the amino terminus codon of the target protein. The histidine "block" of the expressed fusion protein promotes very tight binding to immobilized metal ions and permits rapid purification of the recombinant protein by immobilized metal ion affinity chromatography. The histidine leader sequence is then cleaved at the specific proteolysis site by treatment of the purified protein with thrombin, and the geranylgeranyl diphosphate synthase again purified by immobilized metal ion affinity chromatography, this time using a shallower imidazole gradient to elute the recombinant synthases while leaving the histidine block still adsorbed. This overexpression-purification system has high capacity, excellent resolving power and is fast, and the chance of a contaminating *E. coli* protein exhibiting similar binding behavior (before and after thrombin proteolysis) is extremely small.

As will be apparent to those skilled in the art, any plasmid vectors containing replicon and control sequences that are derived from species compatible with the host cell may also be used in the practice of the invention. The vector usually has a replication site, marker genes that provide phenotypic selection in transformed cells, one or more promoters, and a polylinker region containing several restriction sites for insertion of foreign DNA. Plasmids typically used for transformation of *E. coli* include pBR322, pUC18, pUC19, pUC118, pUC119, and Bluescript M13, all of which are described in sections 1.12-1.20 of Sambrook et al., *supra*. However, many other suitable vectors are available as well. These vectors contain genes coding for ampicillin and/or tetracycline resistance which enables cells transformed with these vectors to grow in the presence of these antibiotics.

The promoters most commonly used in prokaryotic vectors include the β -lactamase (penicillinase) and lactose promoter systems (Chang et al. *Nature*, 375:615 [1978]; Itakura et al., *Science*, 198:1056 [1977]; Goeddel et al., *Nature*, 281:544 [1979]) and a tryptophan (trp) promoter system (Goeddel et al., *Nucl. Acids Res.*, 8:4057 [1980]; EPO Appl. Publ. No. 36,776), and the alkaline phosphatase

systems. While these are the most commonly used, other microbial promoters have been utilized, and details concerning their nucleotide sequences have been published, enabling a skilled worker to ligate them functionally into plasmid vectors (see Siebenlist et al., *Cell*, 20:269 [1980]).

5 Many eukaryotic proteins normally secreted from the cell contain an endogenous secretion signal sequence as part of the amino acid sequence. Thus, proteins normally found in the cytoplasm can be targeted for secretion by linking a signal sequence to the protein. This is readily accomplished by ligating DNA encoding a signal sequence to the 5' end of the DNA encoding the protein and then
10 expressing this fusion protein in an appropriate host cell. The DNA encoding the signal sequence may be obtained as a restriction fragment from any gene encoding a protein with a signal sequence. Thus, prokaryotic, yeast, and eukaryotic signal sequences may be used herein, depending on the type of host cell utilized to practice the invention. The DNA and amino acid sequence encoding the signal sequence
15 portion of several eukaryotic genes including, for example, human growth hormone, proinsulin, and proalbumin are known (see Stryer, *Biochemistry* W.H. Freeman and Company, New York, NY, p. 769 [1988]), and can be used as signal sequences in appropriate eukaryotic host cells. Yeast signal sequences, as for example acid phosphatase (Arima et al., *Nuc. Acids Res.*, 11:1657 [1983]), α -factor, alkaline
20 phosphatase and invertase may be used to direct secretion from yeast host cells. Prokaryotic signal sequences from genes encoding, for example, LamB or OmpF (Wong et al., *Gene*, 68:193 [1988]), MalE, PhoA, or beta-lactamase, as well as other genes, may be used to target proteins from prokaryotic cells into the culture medium.

Trafficking sequences from plants, animals and microbes can be employed in
25 the practice of the invention to direct the geranylgeranyl diphosphate synthase proteins of the present invention to the cytoplasm, endoplasmic reticulum, mitochondria or other cellular components, or to target the protein for export to the medium. These considerations apply to the overexpression of geranylgeranyl diphosphate synthase, and to direction of expression within cells or intact organisms
30 to permit gene product function in any desired location.

The construction of suitable vectors containing DNA encoding replication sequences, regulatory sequences, phenotypic selection genes and the geranylgeranyl diphosphate synthase DNA of interest are prepared using standard recombinant DNA procedures. Isolated plasmids and DNA fragments are cleaved, tailored, and ligated

together in a specific order to generate the desired vectors, as is well known in the art (see, for example, Sambrook et al., *supra*).

As discussed above, geranylgeranyl diphosphate synthase variants are preferably produced by means of mutation(s) that are generated using the method of site-specific mutagenesis. This method requires the synthesis and use of specific oligonucleotides that encode both the sequence of the desired mutation and a sufficient number of adjacent nucleotides to allow the oligonucleotide to stably hybridize to the DNA template.

The foregoing may be more fully understood in connection with the following representative examples, in which "Plasmids" are designated by a lower case p followed by an alphanumeric designation. The starting plasmids used in this invention are either commercially available, publicly available on an unrestricted basis, or can be constructed from such available plasmids using published procedures. In addition, other equivalent plasmids are known in the art and will be apparent to the ordinary artisan.

"Digestion", "cutting" or "cleaving" of DNA refers to catalytic cleavage of the DNA with an enzyme that acts only at particular locations in the DNA. These enzymes are called restriction endonucleases, and the site along the DNA sequence where each enzyme cleaves is called a restriction site. The restriction enzymes used in this invention are commercially available and are used according to the instructions supplied by the manufacturers. (See also sections 1.60-1.61 and sections 3.38-3.39 of Sambrook et al., *supra*.)

"Recovery" or "isolation" of a given fragment of DNA from a restriction digest means separation of the resulting DNA fragment on a polyacrylamide or an agarose gel by electrophoresis, identification of the fragment of interest by comparison of its mobility versus that of marker DNA fragments of known molecular weight, removal of the gel section containing the desired fragment, and separation of the gel from DNA. This procedure is known generally. For example, see Lawn et al. (*Nucleic Acids Res.*, 9:6103-6114 [1982]), and Goeddel et al. (*Nucleic Acids Res.*, *supra*).

The following examples merely illustrate the best mode now contemplated for practicing the invention, but should not be construed to limit the invention.

EXAMPLE 1

Isolation of a Full-Length Geranylgeranyl Diphosphate Synthase cDNA Clone

Unless otherwise stated, the following substrates and reagents were utilized in the Examples set forth herein. General molecular biology reagents were obtained from Gibco BRL Life Technologies, Inc., (Rockville, Maryland), Stratagene Cloning Systems, Inc., (La Jolla, California), or New England Biolabs, Inc., (Beverly, Massachusetts), unless otherwise indicated. Biochemicals and standards were obtained from Sigma Chemical Company (St. Louis, Missouri), except as follows. [4-¹⁴C]Isopentenyl diphosphate (54.1 Ci/mol), [α -³²P]dCTP (3000 Ci/mol) and [α -³²P]dATP (3000 Ci/mol) were obtained from DuPont NEN Company (Boston, Massachusetts); [1-³H]₁geranylgeranyl diphosphate (120 Ci/mol) was prepared by a modification of the method of Cramer and Böhm (Cramer, F. and Böhm, W. (1959) *Angew. Chem.*, **71**:775) and was purified as previously described (LaFever, R. E., Stofer Vogel, B. and Croteau, R. (1994) *Arch. Biochem. Biophys.*, **313**:139-149); Farnesyl diphosphate was obtained from American Radiolabeled Chemicals Inc. (St. Louis, Missouri); and Geranylgeraniol and geranylinalool were obtained from Kuraray Co. and American Tokyo Kasei, Inc., respectively.

Unless otherwise stated, the following cell cultures were utilized in the Examples set forth herein. *T. canadensis* suspension-cultured cells were initiated from embryos and maintained as previously described, and the growth and paclitaxel content of the cells were monitored as before (Hezari, M., Ketchum, R.E.B., Gibson, D.M. and Croteau, R. (1997) *Arch. Biochem. Biophys.*, **337**:185-190). *Escherichia coli* strains LE392, XL1-Blue, and XL1-Blue MRF¹ were used for standard molecular biology procedures. *E. coli* JM109 (λ CC) (unpublished, chloramphenicol resistant strain containing *cre* expressed on a λ lysogen) and the yeast/*E. coli* phage λ expression vector λ PG15 (Brunelli, J.P. and Pall, M.L. (1993) *Yeast*, **9**:1309-1318) were gifts from Dr. M. Pall, Washington State University. *Saccharomyces cerevisiae* strain ANY119 was a generous gift from Dr. S. Ferro-Novick, Howard Hughes Medical Institute, Yale University (Jiang, Y., Proteau, P., Poulter, D. and Ferro-Novick, S. (1995) *J. Biol. Chem.*, **270**:21793-21799), and the expression strain INVSc1 was purchased from Invitrogen. The yeast expression vector pYeDP60 (Pompon, D., Benedicte, L., Bronine, A. and Urban, P. (1996) *Methods Enzymol.*, **272**:51-64) was kindly provided by Dr. D. Pompon, CNRS, Université Pierre et Marie Curie, Gif-sur-Yvette, France.

A phage cDNA library from induced *T. canadensis* cells was prepared in λ PG15. Total RNA was isolated using an RNA Maxi kit (Qiagen) from 14-day-old suspension cell cultures which had been induced with 200 μ M methyl jasmonate 7 d prior to harvest by filtration. PolyA⁺ RNA was prepared by chromatography on oligo(dT)-cellulose (Pharmacia Biotech, Piscataway, New Jersey). The cDNA library was synthesized using a λ ZAP-cDNA synthesis kit and ZAP-cDNA gigapack III gold cloning kit (Stratagene) by following the manufacturer's instructions, except that λ PG15 replaced λ ZAP as the cloning vector.

A geranylgeranyl diphosphate synthase cDNA was cloned in the following manner. An initial PCR product was amplified using 150 pmol/reaction of a reverse degenerate primer (SEQ ID NO:3), which corresponded to part of a specific amino acid sequence which was conserved among certain acetyltransferase enzymes. This primer fortuitously hybridized to two different regions of a geranylgeranyl diphosphate synthase mRNA. PCR was carried out by heating the reaction mixture to 94°C for 1 minute, lowering the temperature to 42°C for 1 minute, then raising the temperature to 74°C for 2 minutes. This temperature profile was repeated for 32 cycles. The resulting 861 bp fragment was ligated into pCR 2.1 Topo (Invitrogen Corporation, San Diego, California) and the recombinant vector was transformed into *E. coli* XL1-Blue cells. Forty-five positive colonies were isolated from which plasmids were purified then sequenced using Amplitaq DNA polymerase and FS cycle sequencing on an ABI prismTM 373 DNA sequencer. It was found that only one isolated plasmid contained an insert sequence (SEQ ID NO:4) resembling geranylgeranyl diphosphate synthases from angiosperm plant species (translated Blast score of 1.0×10^{-46}). When compared to other GGPP synthase sequences, this clone (SEQ ID NO:4) was found to encode the first 194 amino acids of the translated protein in addition to 279 bp of the 5'-UTR.

A 583 bp portion of the initial 861 bp PCR product (extending from nucleotide 279 to nucleotide 861 of the cDNA sequence set forth in SEQ ID NO:4) was used as a hybridization probe to obtain a full-length geranylgeranyl diphosphate synthase cDNA sequence. Thus, a nondegenerate forward primer (SEQ ID NO:5) and a nondegenerate reverse primer (SEQ ID NO:6) were designed which corresponded to nucleotides 279 to 300, and 839 to 861, respectively, of the 861 bp cDNA sequence set forth in SEQ ID NO:4. Nondegenerate forward primer (SEQ ID NO:5) and nondegenerate reverse primer (SEQ ID NO:6) were used to amplify the intervening 583 bp region of the 861 bp cDNA sequence set forth in SEQ ID NO:4

by using approximately 1.0×10^8 molecules of the 861 bp fragment (SEQ ID NO:4) as template along with 5 pmol of each of nondegenerate forward primer (SEQ ID NO:5) and nondegenerate reverse primer (SEQ ID NO:6) in a 100 μ l PCR reaction. The temperature profile and cycling conditions were as given above, except that the annealing temperature was raised from 42°C to 50°C.

The resulting, gel purified, amplified cDNA fragment was then labeled with [α - 32 P]ATP by the random hexamer method (Sambrook, J., Fritsch, E. F. and Maniatis, T. (1989) *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY) and used to probe the *T. canadensis* cDNA library, containing approximately 80,000 independent clones. After two rounds of purification, 16 positive clones were excised, *in vivo*, as the plasmid pYPGE15 by infecting *E. coli* JM109 (λ CC). Sequencing revealed that five of the 16 independent isolates each encoded a protein which, based on sequence comparison to other reported GGPP synthases (comparison at the protein level by translated Blast search gave a smallest sum probability of 1.1×10^{-140}), was identified as geranylgeranyl diphosphate synthase.

The sequence of four of the five cDNA clones was identical and is set forth in SEQ ID NO:1. One full-length coding region, free of stop codons, was found beginning at a methionine codon beginning 308 bp from the 5'-terminus of the sequence set forth in SEQ ID NO:1, and ending at a UGA codon at nucleic acid residues 1487 to 1489 of the sequence set forth in SEQ ID NO:1, thereby yielding a coding region of 1182 bp with a 5'-UTR of 308 bp and a 3'-UTR of approximately 400 bp.

When compared with other reported, plant-derived GGPP synthases, the deduced amino acid sequence of this gymnosperm enzyme open reading frame shows reasonable similarity throughout nearly the entire coding region, including the conserved aspartate and arginine residues which have been shown to be important in substrate binding and catalysis (Ashby, M.N. and Edwards, P.A. (1990) *J. Biol. Chem.*, 265:13157-13164; Joly, A. and Edwards, P.A. (1993) *J. Biol. Chem.*, 268:26983-26989; Tarshis, L.C., Proteau, P.J., Kellogg, B.A., Sacchettini, J.C. and Poulter, C.D. (1996) *Proc. Natl. Acad. Sci. USA*, 93:15018-15023; Song, L. and Poulter, C.D. (1994) *Proc. Natl. Acad. Sci. USA*, 91:3044-3048). Pairwise comparisons of the *T. canadensis* GGPP synthase (SEQ ID NO:2) with the corresponding sequences from a variety of other plant species reveal amino acid identities in the range of 45 to 64%. It is important to note, however, that the

majority of the putative GGPP synthase clones from other plants have been identified only by sequence comparison and not by functional expression of the relevant activity. Although it seems likely that the clones that have not been authenticated by expression do encode GGPP synthases, evolutionary studies suggest that short chain prenyltransferases can not be easily grouped by function based on sequence analysis alone (Chen, A., Kroon, P. A. and Poulter, C. D. (1994) *Protein Sci.*, 3:600-607). Of the six defined *Arabidopsis thaliana* GGPP synthase sequences, only two have been characterized biochemically (Zhu, X.F., Suzuki, K., Saito, T., Okada, K., Tanaka, K., Nakagawa, T., Matsuda, H. and Kawamukai, M. (1997) *Plant Mol. Biol.*, 35:331-341; Zhu, X.F., Suzuki, K., Okada, K., Tanaka, K., Nakagawa, T., Kawamukai, M. and Matsuda, H. (1997) *Plant Cell Physiol.*, 38:357-361), and of the remaining GGPP synthase cDNAs of plant origin, only those from *Capsicum annuum* (Kuntz, M., Römer, S., Suire, C., Hugueney, P., Weil, J. H., Schantz, R. and Camara, B. (1992) *Plant J.*, 2:25-34) and *Sinapis alba* (Bonk, M., Hoffman, B., Von Lintig, J., Schledz, M., Al-Babili, S., Hobeika, E., Kleinig, H. and Beyer, P. (1997) *Eur. J. Biochem.*, 247:942-950) have been confirmed by functional expression of prenyltransferase activity.

Evaluation of the relatedness of the GGPP synthases of plant origin (FIGURE 3) indicates that the GGPP synthase sequence disclosed herein (SEQ ID NO:2), the first GGPP synthase sequence from a gymnosperm, bears a closer relationship to GGPP synthases from angiosperms than do two of the clones from *A. thaliana*, Arth2 and Arth3. This is due not only in part to the highly variable transit peptide region characteristic of these enzymes (Chen, A., Kroon, P.A. and Poulter, C.D. (1994) *Protein Sci.*, 3:600-607), but also to the fact that the Arth3 sequence lacks some key areas of amino acid conservation.

EXAMPLE 2

Generation of GGPP Synthase Expression Constructs and Complementation Assays in Yeast.

All known GGPP synthase sequences of plant origin appear to encode a transit peptide for organellar compartmentation of this prenyltransferase (Kleinig, H. (1989) *Annu. Rev. Plant Physiol. Plant Mol. Biol.*, 40:39-59; Chen, A., Kroon, P.A. and Poulter, C.D. (1994) *Protein Sci.*, 3:600-607). Many of these enzymes have been shown to be localized to plastids (Kuntz, M., Römer, S., Suire, C., Hugueney, P., Weil, J.H., Schantz, R. and Camara, B. (1992) *Plant J.*, 2:25-34; Bonk, M., Hoffman,

B., Von Lintig, J., Schledz, M., Al-Babili, S., Hobeika, E., Kleinig, H. and Beyer, P. (1997) *Eur. J. Biochem.*, **247**:942-950; Laferrière, A. and Beyer, P. (1991) *Biochem. Biophys. Acta*, **1077**:167-172), although at least one, from *A. thaliana*, is targeted specifically to mitochondria (Zhu, X.F., Suzuki, K., Saito, T., Okada, K., Tanaka, K., Nakagawa, T., Matsuda, H. and Kawamukai, M. (1997) *Plant Mol. Biol.*, **35**:331-341). Since it was assumed that the *T. canadensis* GGPP synthase cDNA likewise would encode an organellar transit peptide, and that the resulting preprotein would likely be less catalytically efficient than the mature, proteolytically processed form, the deduced amino acid sequence of the putative, *Taxus* GGPP synthase (SEQ ID NO:2) was compared to angiosperm GGPP synthase sequences in order to identify the N-terminal and C-terminal boundaries of the mature protein.

The amino acid sequence comparisons were made using the GCG (Genetics Computer Group (1994) Program Manual for the Wisconsin Package, Version 8, Genetics Computer Group, 575 Science Drive, Madison, WI) program Pileup with a blosum 62 comparison matrix. The gap creation and gap extension penalties were 12.0 and 4.0, respectively. These sequence alignments were displayed using the EGCG (Program Manual for the EGCG Package, Peter Rice, The Sanger Centre, Hinxton Hall, Cambridge, CB101RQ, England) program Prettybox with the plurality set at 4.1. Thus, comparison of plant-derived GGPP synthase amino acid sequences with the deduced *T. canadensis* protein (SEQ ID NO:2) showed that high-level conservation begins at F⁹⁹ of the amino acid sequence set forth in SEQ ID NO:2, indicating a logical truncation site at nucleotide 295 (Tr²⁹⁵) of the GGPP synthase cDNA sequence set forth in SEQ ID NO:2; a second site (at nucleotide 313, Tr³¹³) was chosen (six residues downstream) because of the location of the convenient M¹⁰⁵ residue.

PCR primers containing a *Kpn*I site (SEQ ID NO:7) or a *Bam*HI site (SEQ ID NO:8) were designed to the 3'- and 5'-termini, respectively, of the presumptive full-length coding sequence (SEQ ID NO:1). Additionally, a 5'-terminal primer (SEQ ID NO:9) was designed to correspond to a 5'-truncated version of the GGPP synthase protein sequence set forth in SEQ ID NO:2 beginning at Tr²⁹⁵, while a second 5'-terminal primer (SEQ ID NO:10) was designed to correspond to a 5'-truncated version of the GGPP synthase protein sequence set forth in SEQ ID NO:2 beginning at Tr³¹³. The primers set forth in SEQ ID NO:9 and SEQ ID NO:10 were designed in order to express putative mature proteins devoid of the transit peptide. After amplification with *Pfu* DNA polymerase, the three cDNA fragments were ligated into

PCR-Script CAM SK(+) (Stratagene), then sequenced to ensure that no errors had arisen during amplification. The *Bam*HI/*Kpn*I-digested fragment corresponding to each coding sequence was then subcloned into pYeDP60 under the control of the GAL10-CYC1 promoter.

5 The pYeDP60 constructs were transformed into the *S. cerevisiae* mutant ANY119 using the lithium acetate procedure (Treco, D. (1989) in *Current Protocols in Molecular Biology* (Ausubel, F.M., Brent, R., Kingston, R.E., Moore, D.D., Seidman, J.G., Smith, J.A. and White, T.J., Eds.), pp. 13.7.1-13.7.2, John Wiley and Sons, New York), and the transformed yeast were then plated on a synthetic medium
10 containing glucose as the sole carbon source (but lacking uracil) and grown for 4 d at 25°C. Isolated colonies, corresponding to each construct, were then replica streaked onto SGI, N3 and SLI media and grown for 3, 5 or 7 d, respectively, at 25°C or 37°C.

SGI and SLI synthetic media contain, respectively, 20 g/liter glucose (G) or
15 20 g/liter galactose (L) in 1 g/liter bactocasamino acids (Difco), 6.7 g/liter yeast nitrogen base without amino acid (Difco), and 40 mg/liter DL-tryptophan. SGAI and SLAI are identical to SGI and SLI except that 30 mg/liter adenine is added. YPGE complete medium contains 5 g/liter glucose, 10 g/liter yeast extract (Difco), 10 g/liter bactopectone (Difco Laboratories, Inc., Detroit, Michigan), and 3% (by vol) ethanol.
20 YPG(A) and YPL(A), respectively, contain 20 g/liter glucose or 20 g/liter galactose in 10 g/liter yeast extract, 10 g/liter bactopectone, and, when required, 30 mg/liter adenine (A).

The three pYeDP60/*T. canadensis* GGPP synthase constructs were introduced into and expressed in ANY119, an *S. cerevisiae* mutant that is defective
25 for the β -subunit of type II geranylgeranyltransferase. This mutation is lethal at high temperature but can be complemented by increasing the expression level of GGPP synthase (Jiang, Y., Proteau, P., Poulter, D. and Ferro-Novick, S. (1995) *J. Biol. Chem.*, 270:21793-21799). To determine if the *T. canadensis* GGPP synthase forms could be functionally expressed in yeast at levels sufficient to rescue this mutant when
30 grown at the restrictive temperature, the expression of the three constructs was tested on three different carbon sources that differentially regulate GAL10-CYC1 promoter activity (Pompon, D., Benedicte, L., Bronine, A. and Urban, P. (1996) *Methods Enzymol.*, 272:51-64). This promoter is repressed in the presence of glucose (SGI medium), induced in the presence of galactose (SLI medium) and behaves in a neutral
35 manner with glycerol as the sole carbon source (N3 medium).

Isolated transformants bearing each construct (full-length, Tr²⁹⁵ and Tr³¹³), as well as the empty vector (control), were streaked on each carbon source medium and grown at the permissive temperature (25°C) and the restrictive temperature (37°C). At 25°C, each of the transformants grew on SGI and N3 medium after 3d and 5 d, respectively. However, on SLI medium, modest growth was observed only for the control and Tr³¹³ constructs, even after 7 d. From these results, it was concluded that ANY119 uses galactose only poorly as a sole carbon source. At 37°C, no growth was observed on SLI after 7 d; however, on both SGI (3 d) and N3 (5 d), only transformants harboring the full-length and Tr²⁹⁵ constructs showed growth, while no growth was exhibited by transformants bearing the control and Tr³¹³ constructs. These results indicate that both the full-length GGPP synthase clone and the Tr²⁹⁵ truncation rescue the *bet2-1* mutant and that, even under repressed conditions (on SGI), enough leaky expression of GGPP synthase occurs to complement the mutation.

To test the expression of GGPP synthase on galactose as carbon source, each construct was transformed into a yeast strain (INVSc1) that metabolizes this sugar efficiently. These INVSc1 transformants were plated on SLI medium and grown at 30°C for 3 d, whereupon luxuriant growth was observed for the control yeast and that bearing the Tr³¹³ construct, whereas only scanty growth was seen for the yeast bearing the full-length construct; that bearing the Tr²⁹⁵ construct did not grow at all. These results indicate that, when high level expression of the heterologous GGPP synthase is fully induced, the gene is toxic. Furthermore, it can be concluded from both these and the above results that the full-length and Tr²⁹⁵ constructs yield active GGPP synthase but that the shorter Tr³¹³ truncation construct does not.

EXAMPLE 3

Analysis of Expression Level and Toxicity of *Taxus* GGPP Synthase in Yeast

To determine the amount of GGPP synthase protein expressed from each construct, the corresponding transformed INVSc1 cells were grown in large scale YPGE liquid cultures and induced by the addition of galactose, and the soluble proteins were extracted and analyzed by SDS-PAGE. Colonies were inoculated into 30 ml of SGI medium and grown at 30°C for 20 h. One liter of YPGE medium (1% yeast extract, 1% peptone, 0.5% glucose and 3% ethanol) was then inoculated with 20 ml of the SGI starter culture which was grown at 28°C to a concentration of 1.2×10^8 cells/ml. The cultures were then adjusted to 2% (v/v) galactose and grown

to a final density of approximately 4.5×10^8 cells/ml. The cells were harvested by centrifugation at 6700g for 5 min, the supernatant was decanted, and the cell pellets were resuspended in 200 ml of 50 mM Tris buffer (pH 7.6) containing 100 mM KCl.

After centrifugation as above, the cell pellet was resuspended in 80 ml of ice cold 50 mM Tris (pH 7.6) containing 10% (v/v) glycerol, 10 mM $MgCl_2$, 5 mM DTT, and 1 μ g/ml leupeptin (extraction/assay buffer). All subsequent operations were conducted at 0-4°C. Cells were disrupted with 150 ml glass beads using a Biospec Bead-Beater operated at 90 V for 5 min, and the resulting debris was removed by centrifugation at 3000g for 20 min to yield a supernatant that was further clarified by centrifugation at 31,000g for 20 min. The resulting supernatant was used as the enzyme source. Protein concentration was estimated by the method of Bradford (Bradford, M.M. (1976) *Anal. Biochem.*, 72:248-254), and the preparations were evaluated by SDS-PAGE on 10% acrylamide gels (2.1 mg total protein per lane) by the method of Laemmli (Laemmli, U.K. (1970) *Nature*, 227:680-685) followed by silver staining (Blum, H., Beir, H. and Gross, H.J. (1987) *Electrophoresis*, 8:93-99).

The size of the presumptive, mature, recombinant, homodimeric enzyme was determined by gel permeation chromatography using a Pharmacia 16/60 Superdex G-75 column eluted with 25 mM Mopso (pH 7.0) containing 10% (v/v) glycerol, 1% (v/v) ethylene glycol and 100 mM NaCl at a flow rate of 1 ml/min.

A prominent protein band at about 32 kDa was observed only in the extract of the yeast harboring the Tr^{295} construct; this size corresponds to the calculated monomeric size of 32.1 kDa for this truncated GGPP synthase. None of the transformants bearing other constructs yielded extracts with protein banding patterns appreciably different from that of the empty vector control. These results suggest that the Tr^{295} construct is expressed at a high level but that the Tr^{313} truncation and full-length constructs are not sufficiently expressed to afford an observable soluble protein.

The toxicity of the constitutively expressed, recombinant GGPP synthase gene in yeast and in *E. coli* parallels the *in vitro* activity of the enzyme expressed in the truncation series. Thus, the Tr^{295} construct is extremely toxic, the full-length gene (encoding the preprotein) causes a noticeable reduction in growth, whereas the Tr^{313} construct has no effect on cell growth. This toxicity is not observed when the corresponding transformed yeast are grown on glucose or glycerol (uninduced condition), but only when the gene is actively expressed by growth under inducing conditions with galactose as the carbon source. The overexpression of this gene to

produce a functional GGPP synthase probably interferes with metabolism by depleting intracellular pools of FPP, via diversion to GGPP, and thus limiting sterol biosynthesis. Similarly, in *E. coli* when Tr²⁹⁵, or the full-length GGPP synthase clone (SEQ ID NO:1), is expressed under a strong constitutive promoter the cells will not grow. The vector used in these *E. coli* transformation experiments was pYPGE15, the plasmid derived from λ PG15.

Conversely, the complementation of the ANY119 *bet2-1* yeast mutant by GGPP synthase is thought to occur by an increase in the intracellular concentration of GGPP (Jiang, Y., Proteau, P., Poulter, D. and Ferro-Novick, S. (1995) *J. Biol. Chem.*, 270:21793-21799). Interestingly, complementation was observed when the cells were plated on medium containing glucose as the sole carbon source, conditions under which the GAL10-CYC1 hybrid promoter is thought to be fully repressed (Pompon, D., Benedicte, L., Bronine, A. and Urban, P. (1996) *Methods Enzymol.*, 272:51-64). Thus, it appears that there is sufficient leaky expression of this gene to rescue the mutant under these conditions. The fact that Jiang et al. (Jiang, Y., Proteau, P., Poulter, D. and Ferro-Novick, S. (1995) *J. Biol. Chem.*, 270:21793-21799) demonstrated that the level of mutant complementation was dependent on the level of expression of a cloned yeast GGPP synthase, combined with the tight regulation provided by the GAL10-CYC1 promoter, suggests that expression of even very low levels of the Tr²⁹⁵ construct affords an enzyme with adequate catalytic activity to rescue the mutant.

EXAMPLE 4

Product Identification and Characterization of Recombinant GGPP Synthase

To confirm that the protein encoded by the isolated *T. canadensis* cDNA was indeed geranylgeranyl diphosphate synthase, prenyltransferase assays were performed with the corresponding yeast extracts using [4-¹⁴C]IPP and FPP as co-substrates under conditions where background activity from endogenous yeast GGPP synthase was negligible.

The standard assay for prenyltransferase activities was performed with 21 mg protein in a total volume of 100 μ l of the extraction/assay buffer disclosed in Example 3. DMAPP (200 μ M), GPP (200 μ M) or FPP (200 μ M), and the homoallylic co-substrate [4-¹⁴C]IPP (50 μ M), were added as appropriate for the assay, and the reaction mixtures were incubated at 31°C for 20 min. The reaction was quenched by the addition of 300 μ l of methanol:conc. HCl (4:1, v/v), and the allylic

diphosphate products were solvolyzed (50, 51) upon further incubation at 42°C for 20 min. The resulting solvolysis products were extracted twice with 1 ml pentane, and were either analyzed by liquid scintillation counting (in toluene:ethanol (7:3, v/v) containing 0.4% Omnifluor (DuPont NEN); ¹⁴C counting efficiency = 96.0%) or concentrated on ice under a gentle stream of Ar to ~100 ml for further analysis.

For radio-TLC analysis, samples were mixed with 10 mg each of geranylgeraniol (all *trans*), geranylinalool (mixed geometric isomers), farnesol and geraniol and spotted on Whatman MKC 18F reversed phase plates that were developed with acetonitrile:acetone:water (15:4:1, v/v/v) and visualized with I₂ vapor. Bands corresponding to the standards were scraped into scintillation vials for counting. For radio-GC analysis, the above pentane extract was diluted with 200 ml of an 8% ethereal solution of the internal standards before concentration on ice. Product identity was confirmed by radio-GC (Satterwhite, D.M. and Croteau, R. (1988) *J. Chromatogr.*, 452:61-73) coincidence with the authentic standard on a 12 ft x 0.125 in. polydimethylsiloxane column (15% SE-30 on 80/100-mesh Chromasorb WHP; (Alltech, Inc., Nicholasville, Kentucky), with He as carrier and temperature programming from 150°C (1 min hold) to 240°C (20 min hold) at 8°C/min.

For kinetic evaluations, the protein concentrations and incubation times for the assays were reduced to 4 mg and 7.5 min, respectively, to ensure linearity, and the concentrations of IPP (0.5-100 mM), FPP (0.05-200 mM) and Mg²⁺ (0.01-1000 mM) were independently varied in assays in which the remaining reactants were maintained at saturation. Double reciprocal plots were constructed for each data set and the equation of the best-fit line ($r^2 > 0.97$) was determined (KaleidaGraph, version 3.08, Synergy Software, Reading, PA). For evaluation of relative velocities, DMAPP, GPP and FPP were compared as the allylic co-substrate at concentrations of 12.5 mM and 25 mM.

Only the enzyme preparation from yeast expressing the Tr²⁹⁵ construct was highly active; when compared on a protein basis, the preprotein (full-length construct) was only 12% as active as the truncated form expressed from Tr²⁹⁵, whereas the enzyme expressed from truncation Tr³¹³ was not detectably active.

Expression of highly active *T. canadensis* GGPP synthase appears to be dependent on removal of the transit peptide in the Tr²⁹⁵ construct. This truncation was designed based upon sequence homology, rather than upon predictive methods for the cleavage site (Keegstra, K., Olsen, J.J. and Theg, S.M. (1989) *Annu. Rev. Plant Physiol. Plant Mol. Biol.*, 40:471-501; von Heijne, G., Steppuhn, J. and

Herrmann, R.G. (1989) *Eur. J. Biochem.*, **180**:535-545). Even though the full-length preprotein was apparently much less active, and the Tr³¹³ truncated protein was apparently inactive, neither of these proteins was observed to be efficiently expressed, as determined by SDS-PAGE analysis of the protein extracts of the corresponding transformed yeast. Thus, because comparative specific activities could not be easily determined, it is premature to conclude that the preprotein is inherently less active than the processed, mature form, or that the truncation site of the Tr³¹³-expressed protein extends too far into the conserved region of the enzyme to yield a catalytically active species.

Analysis, by reversed phase TLC, of the solvolysis products of the prenyltransferase reaction (utilizing [4-¹⁴C]IPP plus FPP as substrates) catalyzed by the truncated enzyme expressed from the Tr²⁹⁵ construct revealed that 97% of the total radioactivity coincided with the geranylgeraniol and geranyllinalool standards (see FIGURE 2), as expected. Radio-GC analysis (FIGURE 4) of the reaction products indicated the presence of two components, coincident with all *trans* geranyllinalool (major component) and geranylgeraniol, respectively, and a third (middle peak) with relative retention time consistent with that of geranylnerol. This observed product distribution is consistent with that expected for the acid-catalyzed solvolysis of allylic diphosphates (Tidd, B.K. (1971) *J. Chem. Soc. (B)*, **1971**:1168-1176), such as GGPP, confirming that a cDNA encoding GGPP synthase had been obtained.

Kinetic evaluation of the GGPP synthase by double reciprocal plotting afforded a K_m value for IPP of 7 mM, for FPP of 6 mM, and for the required divalent metal ion (Mg^{2+}) of 35 mM; Mn^{2+} did not support catalysis by this enzyme. These K_m values are in the range of those reported for other GGPP synthases, some of which, unlike this enzyme from Canadian yew, are able to utilize either Mn^{2+} or Mg^{2+} as cofactor although rarely with comparable efficiency (West, C.A., Dudley, M.W. and Dueber, M.T. (1979) *Recent Adv. Phytochem.*, **13**:163-198; West, C.A. (1981) *in* Biosynthesis of Isoprenoid Compounds (Porter, J.W. and Spurgeon, S.L., Eds.), Vol. 1, pp. 375-411, Wiley, New York, NY; Gershenzon, J. and Croteau, R. (1993) *in* Lipid Metabolism in Plants (Moore, T.S., Jr., Ed.), pp. 339-388, CRC Press, Boca Raton, FL; Ogura, K. and Koyama, T. (1998) *Chem. Rev.*, in press). The relative velocities of the reaction with the three possible allylic co-substrates, DMAPP, GPP, and FPP, were examined at concentrations of 12.5 and 25 mM, with IPP and Mg^{2+} concentrations at saturation, and shown to be DMAPP = 33%, FPP = 66%, and GPP

= 100%. The utilization of the C₅ and C₁₀ allylic co-substrates, in addition to FPP, has been observed previously with other GGPP synthases which, based on the above properties, the enzyme from *T. canadensis* appears to resemble (Laferrière, A. and Beyer, P. (1991) *Biochem. Biophys. Acta*, 1077:167-172; Ogura, K. and Koyama, T. (1998) *Chem. Rev.*, in press; Brinkhaus, F.L. and Rilling, H.C. (1988) *Arch. Biochem. Biophys.*, 266:607-612). Some GGPP synthases (i.e., farnesyl transferase) do not utilize DMAPP, and use GPP as the allylic cosubstrate only inefficiently (West, C.A., Dudley, M.W. and Dueber, M.T. (1979) *Recent Adv. Phytochem.*, 13:163-198).

Gel permeation chromatography on a calibrated Superdex G-75 (Pharmacia, Biotech, Piscataway, New Jersey) column yielded an elution volume corresponding to a molecular weight of approximately 60,000 for the GGPP synthase Tr²⁹³ truncated protein which, along with the predicted size of 32.1 kDa and the results of SDS-PAGE, indicate that the enzyme exists as a functional dimer. This observation is consistent with the size and the subunit architecture determined for the native GGPP synthases from other sources (West, C.A., Dudley, M.W. and Dueber, M.T. (1979) *Recent Adv. Phytochem.*, 13:163-198; Laferrière, A. and Beyer, P. (1991) *Biochem. Biophys. Acta*, 1077:167-172; Dogbo, O. and Camara, B. (1987) *Biochem. Biophys. Acta*, 920:140-148; Ogura, K. and Koyama, T. (1998) *Chem. Rev.*, in press).

EXAMPLE 5

Changes in GGPP Synthase and Taxadiene Synthase Enzyme Activity and mRNA Levels in Response to Methyl Jasmonate

Suspension cell cultures were treated with methyl jasmonate 7 d after subculture and harvested at 8, 12, 24, 48 or 168 h after elicitation, or immediately before induction. During this 7 d induction period, the wet cell mass increased by about 10% and the paclitaxel concentration in the medium (where the majority of the taxoids accumulate) rose from 2.5 mg/l to 32 mg/l, with the greatest increase occurring after 48 h. The concentration of paclitaxel was measured by calibrated HPLC with UV detection as described in Hezari et al, *Arch. Biochem. Biophys.*, 337:185-190 (1997).

The regulation of gene expression over the time course of induction was examined by RNA-blot analysis of total RNA isolated from the cells using probes for GGPP synthase and taxadiene synthase, the first two enzymes of the paclitaxel pathway leading from primary metabolism (i.e., from IPP and DMAPP). Total RNA was isolated from *T. canadensis* suspension cell cultures using the method set forth in

Example 1. Equivalent amounts of RNA (14.5 mg) from cells that had been harvested 8, 12, 24, 48, and 168 h after methyl jasmonate induction, as well as RNA isolated from non-induced cells (0 h), were separated by electrophoresis on a formaldehyde-denaturing agarose gel, along with RNA size standards (Promega Corporation, Madison, Wisconsin). The separated RNA was blotted to nylon membrane by capillary action and then fixed by UV irradiation. Radiolabeled probes corresponding to the full length GGPP synthase coding region (nucleotide 308 to nucleotide 1489 of the nucleic acid sequence set forth in SEQ ID NO:1), and to an internal fragment (nucleotides 173 to 1875 inclusive) of the taxadiene synthase cDNA reported in Wildung, M. R. and Croteau, R. (1996) *J. Biol. Chem.*, 271:9201-9204, generated by PCR, were synthesized using a Ready-To-Go probe synthesis kit (Pharmacia Biotech, Piscataway, New Jersey), then purified using a Sephadex G-50 spin column (Pharmacia). The blot was incubated sequentially with each probe for 16 h at 65°C, then washed twice with 2 x SSC at room temperature, and then thrice with 0.5 x SSC at 65°C. The blot was imaged using a Bio-Rad GS-525 Molecular Imager* System and Molecular Analyst version 2.1 software.

A rapid increase in the steady state mRNA levels for both GGPP synthase and taxadiene synthase was observed at 8 h, and these levels remained significantly elevated through at least 48 h before decline. However, even after 168 h, the steady state levels of these transcripts were discernibly higher than the non-induced control.

The same *T. canadensis* cell cultures used for RNA blot analysis were also used to determine the relative activities of GGPP synthase and taxadiene synthase over the course of methyl jasmonate induction of paclitaxel biosynthesis. One gram (fresh wt.) of cells corresponding to each time point were ground to a fine powder in liquid nitrogen then placed in 5 ml of 30 mM Hepes buffer (pH 7.9) containing 15 mM MgCl₂, 5 mM sodium ascorbate, 5 mM Na₂S₂O₅, 5 mM dithiothreitol, 10% (v/v) glycerol, 1% (w/v) polyvinylpyrrolidone (*M_r* ~10,000) and 0.3 g each of polyvinylpolypyrrolidone and Amberlite XAD-4, and agitated gently for 30 min at 4°C. Particulate material and cellular debris were removed from the homogenates by centrifugation, first at 3000g, then at 31,000g, for 20 min at 4°C. Protein concentration in the supernatant used as the enzyme source was estimated by the method of Bradford (Bradford, M.M. (1976) *Anal. Biochem.* 72:248-254).

GGPP synthase activity was determined by the standard prenyltransferase assay described in Example 4, except that 100 µl of crude extract (150 µg protein) isolated from *T. canadensis* cell cultures was used as the enzyme source and the

reactions were incubated for 10 min. Taxadiene synthase activity was determined by measuring the Mg^{2+} -dependent conversion of $[1-^3H_1]$ geranylgeranyl diphosphate (15 μM) to the olefin product as described in Hezari, M., Lewis, N.G. and Croteau, R. (1995) *Arch. Biochem. Biophys.*, **322**:437-444; Hezari, M., Ketchum, R.E.B.,
5 Gibson, D.M. and Croteau, R. (1997) *Arch. Biochem. Biophys.*, **337**:185-190. In this assay, 500 μl of the crude extract (750 μg protein) was incubated at 31°C for 1 h.

Activity for the first two pathway enzymes also increased over time in response to methyl jasmonate (FIGURE 5). Following a short induction period, the activity levels for both GGPP synthase and taxadiene synthase rose steadily to 48 h,
10 with relatively little change thereafter. This kinetic behavior is consistent with the initiation of steady production rates of paclitaxel at about 48 h. In comparing the northern blot analyses to the enzyme activity curves (FIGURE 5), it is apparent that there is a delay of at least a day between the peak steady state mRNA levels and the peak of activities for both corresponding synthases, which may suggest that these
15 messages are translated with low efficiency or that additional levels of post-transcriptional or post-translational control are in operation. The time frame for this induced response of *Taxus* cells to methyl jasmonate is comparable to that of elicitor-induced sesquiterpenoid phytoalexin production in tobacco (Facchini, P.J. and Chappell, J. (1992) *Proc. Natl. Acad. Sci. USA*, **89**:11088-11092; Vögeli, U. and
20 Chappell, J. (1988) *Plant Physiol.*, **88**:1291-1296; Threlfall, D.R. and Whitehead, I.M. (1988) *Phytochemistry*, **27**:2567-2580) or diterpenoid phytoalexin production in castor bean (West, C.A., Lois, A.F., Wickham, K.A. and Ren, Y.-Y. (1990) *Recent Adv. Phytochem.*, **24**:219-248), and only slightly faster, but of shorter duration, than wound-induced oleoresin terpene production in grand fir (Steele, C. L., Katoh, S.,
25 Bohlmann, J. and Croteau, R. (1998) *Plant Physiol.*, **116**, 1497-1504).

In comparing the activity levels of GGPP synthase and taxadiene synthase derived from non-induced and induced cells (FIGURE 5), it is apparent that GGPP synthase is present in substantial excess. However, it should be noted that these synthase activities were measured in crude extracts which may not accurately reflect
30 *in vivo* differences in activity levels. Nevertheless, based on the magnitude of the difference, it seems unlikely that the prenyltransferase is rate limiting in either constitutive or induced paclitaxel production. In considering future approaches for biological production of the drug, however, the fact that the *T. canadensis* GGPP synthase cDNA is cloned and can be functionally expressed in a eukaryotic host does
35 allow for the eventual possibility of increasing paclitaxel yields in genetically

engineered *Taxus* cells in which genes for slow steps of the pathway are overexpressed and where the maintenance of a high level supply of GGPP may be required.

EXAMPLE 6

5 Isolation of a GGPP Synthase cDNA Clone (SEQ ID NO:11) from *Taxus cuspidata*

A phage cDNA library from induced *T. cuspidata* cells was prepared in λPG15. Total RNA was isolated using an RNA Maxi kit (Qiagen N.V., Amsterdam, The Netherlands) from 14-day-old suspension cell cultures which had been induced
10 with 200 μM methyl jasmonate 7 d prior to harvest by filtration. PolyA⁺ RNA was prepared by chromatography on oligo(dT)-cellulose (Pharmacia Biotech). The cDNA library was synthesized using a λZAP-cDNA synthesis kit and ZAP-cDNA gigapack III gold cloning kit (Stratagene) by following the manufacturer's instructions, except that λPG15 replaced λZAP as the cloning vector.

15 A partial-length cDNA clone (SEQ ID NO:11) encoding a GGPP synthase (SEQ ID NO:12) was amplified by PCR using the primers set forth in SEQ ID NO:7 and SEQ ID NO:9. The *T. cuspidata* GGPP synthase partial cDNA (SEQ ID NO:11) encodes the mature form of the *T. cuspidata* GGPP synthase enzyme, i.e., the form of the enzyme that lacks the transit peptide at the amino terminus. The deduced amino
20 acid sequence of the *T. cuspidata* enzyme (SEQ ID NO:12) is identical to the mature form of the *T. canadensis* enzyme. At the nucleotide level, the *T. cuspidata* cDNA (SEQ ID NO:11) is almost identical (98.6% similarity) to the *T. canadensis* GGPP synthase cDNA (SEQ ID NO:1).

EXAMPLE 7

25 Physical Properties of GGPP Synthase Proteins Isolated from Various *Taxus* Species

Table 1 sets forth certain physical properties of GGPP synthase proteins isolated from the following *Taxus* species: *T. canadensis*; *T. brevifolia*; *T. cuspidata* and *T. haccata*.

Table 1

Native Molecular Weight of Homodimer	60,000±2,000
K _m ^{IPP}	7±1µM
K _m ^{FPP}	6±1µM
K _m ^{Mg²⁺}	35±3µM
pH optimum	7.5±0.2
Cosubstrate Utilization Ratio GPP:FPP:DMAP	3:2:1

Some authorities regard all eight species within the genus *Taxus*, including the foregoing *Taxus* species, as being so similar that they are not distinct species, but are actually geographic variants of the same species. See, *The Yew Tree: Biography of a Species*, page 57, H. Hartzell Jr., Hulogosi Press, Eugene, Oregon (1991); Voliotis, D. *Historical and Environmental Significance of the Yew (Taxus baccata L.)*. Israel Journal of Botany, 35:1-58 (1986); Bolsinger, C. and Jaramillo, A.E., "*Taxus brevifolia* Nutt. *Pacific Yew*" in *Silvics of Forest Trees of North America*. Pacific Northwest Research Station, pp 15-24 (1990).

EXAMPLE 8

Hybridization of *T. canadensis* GGPP Synthase cDNA (SEQ ID NO:1) to Other Nucleic Acid Sequences of the Present Invention

Utilizing Northern blot analysis, the GGPP synthase cDNA clone set forth in SEQ ID NO:1, or its complementary sequence, is capable of hybridizing to other nucleic acids of the present invention under the following conditions: hybridization in 5 X SSC at 65°C for 16 hours. Once hybridized under the foregoing hybridization conditions, the GGPP synthase cDNA clone set forth in SEQ ID NO:1, or its complementary sequence, is capable of remaining hybridized to other nucleic acids of the present invention under the following wash conditions: two washes in 2 X SSC at room temperature (20°C to 25°C) for 15 minutes per wash, followed by two washes in 0.2 X SSC at 65°C for 20 minutes per wash.

When screening a cDNA library, the GGPP synthase cDNA clone set forth in SEQ ID NO:1, or its complementary sequence, is capable of hybridizing to other nucleic acids of the present invention under the following conditions: hybridization in 3 X SSC at 65°C for 16 hours. Once hybridized under the foregoing hybridization conditions, the GGPP synthase cDNA clone set forth in SEQ ID NO:1, or its complementary sequence, is capable of remaining hybridized to other nucleic acids of the present invention under the following wash conditions: two washes in 2 X SSC at room temperature (20°C to 25°C) for 20 minutes per wash, followed by one wash in 0.5 X SSC at 55°C for 30 minutes.

10 The ability of the nucleic acid molecules of the present invention to hybridize, and to remain hybridized, to the nucleic acid sequence set forth in SEQ ID NO:1, or to the complementary sequence of the nucleic acid sequence set forth in SEQ ID NO:1, can be determined utilizing the technique of hybridizing radiolabelled nucleic acid probes to nucleic acids immobilized on nitrocellulose filters or nylon membranes as set forth, for example, at pages 9.52 to 9.55 of Molecular Cloning, A Laboratory Manual (2nd edition), J. Sambrook, E.F. Fritsch and T. Maniatis eds, the cited pages of which are incorporated herein by reference.

15 In addition to the nucleic acid sequences set forth in SEQ ID NO:1 and SEQ ID NO:11, examples of representative nucleic acid sequences of the present invention that encode a *Taxus* GGPP synthase and which hybridize to the complementary sequence of the nucleic acid sequence disclosed in SEQ ID NO:1 under the foregoing hybridization conditions (and which remain hybridized under any of the foregoing wash conditions) are set forth in SEQ ID NO:13; SEQ ID NO:15; SEQ ID NO:17; SEQ ID NO:19; SEQ ID NO:21; SEQ ID NO:23; and SEQ ID NO:25.

20 In addition to the protein sequences set forth in SEQ ID NO:2 and SEQ ID NO:12, examples of representative GGPP synthase proteins of the present invention are set forth in SEQ ID NO:27; SEQ ID NO:28; SEQ ID NO:29; SEQ ID NO:30; SEQ ID NO:31; SEQ ID NO:32; SEQ ID NO:33 and SEQ ID NO:34.

25 While the preferred embodiment of the invention has been illustrated and described, it will be appreciated that various changes can be made therein without departing from the spirit and scope of the invention.

The embodiments of the invention in which an exclusive property or privilege is claimed are defined as follows:

1. An isolated nucleic acid molecule encoding a geranylgeranyl diphosphate synthase protein from a *Taxus* species.
2. An isolated nucleic acid molecule of Claim 1 encoding a geranylgeranyl diphosphate synthase protein from a *Taxus* species selected from the group consisting of *Taxus canadensis*, *Taxus brevifolia*, *Taxus cuspidata* and *Taxus baccata*.
3. An isolated nucleic acid molecule of Claim 1 encoding a geranylgeranyl diphosphate synthase protein from a *Taxus* species selected from the group consisting of *Taxus canadensis* and *Taxus cuspidata*.
4. An isolated nucleic acid molecule of Claim 1 having the nucleotide sequence set forth in SEQ ID NO:1 or SEQ ID NO:11.
5. An isolated nucleic acid molecule of Claim 1 which encodes the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:12.
6. An isolated nucleic acid molecule that is capable of hybridizing to the nucleic acid sequence set forth in SEQ ID NO:1, or to the complementary sequence of the nucleic acid sequence set forth in SEQ ID NO:1, under the cDNA library hybridization conditions set forth in Example 8, said isolated nucleic acid molecule being capable of remaining hybridized to the nucleic acid sequence set forth in SEQ ID NO:1, or to the complementary sequence of the nucleic acid sequence set forth in SEQ ID NO:1, under the cDNA library wash conditions set forth in Example 8.
7. An isolated, recombinant *Taxus* geranylgeranyl diphosphate synthase protein.
8. An isolated recombinant protein of Claim 7, said protein being isolated from a plant species selected from the group consisting of *Taxus canadensis*, *Taxus brevifolia*, *Taxus cuspidata* and *Taxus baccata*.

9. An isolated recombinant protein of Claim 7, said protein being isolated from the group consisting of *Taxus canadensis* and *Taxus cuspidata*.

10. An isolated recombinant protein of Claim 7 having the amino acid sequence of the protein set forth in SEQ ID NO:2 or SEQ ID NO:12.

11. A replicable expression vector comprising a nucleic acid sequence encoding a geranylgeranyl diphosphate synthase from a *Taxus* species.

12. A replicable expression vector of Claim 11 comprising a nucleic acid sequence encoding a geranylgeranyl diphosphate synthase from a *Taxus* species selected from the group consisting of *Taxus canadensis*, *Taxus brevifolia*, *Taxus cuspidata* and *Taxus baccata*.

13. A replicable expression vector of Claim 12 comprising a nucleic acid sequence encoding a geranylgeranyl diphosphate synthase from a *Taxus* species selected from the group consisting of *Taxus canadensis*, and *Taxus cuspidata*.

14. A replicable vector comprising a nucleic acid sequence that is capable of hybridizing to the nucleic acid sequence set forth in SEQ ID NO:1, or to the complementary sequence of the nucleic acid sequence set forth in SEQ ID NO:1, under the cDNA library hybridization conditions set forth in Example 8, said hybridizing nucleic acid sequence being capable of remaining hybridized to the nucleic acid sequence set forth in SEQ ID NO:1, or to the complementary sequence of the nucleic acid sequence set forth in SEQ ID NO:1, under the cDNA library wash conditions set forth in Example 8.

15. A host cell comprising a vector of Claim 11.

16. A host cell of Claim 15 wherein said host cell is a *Taxus* cell.

17. A method of increasing geranylgeranyl diphosphate synthase activity in a suitable host cell comprising introducing into said host cell an expression vector of Claim 11 under conditions enabling expression of said protein encoded by said vector.

18. The method of Claim 17 wherein said host cell is a *Taxus* cell.

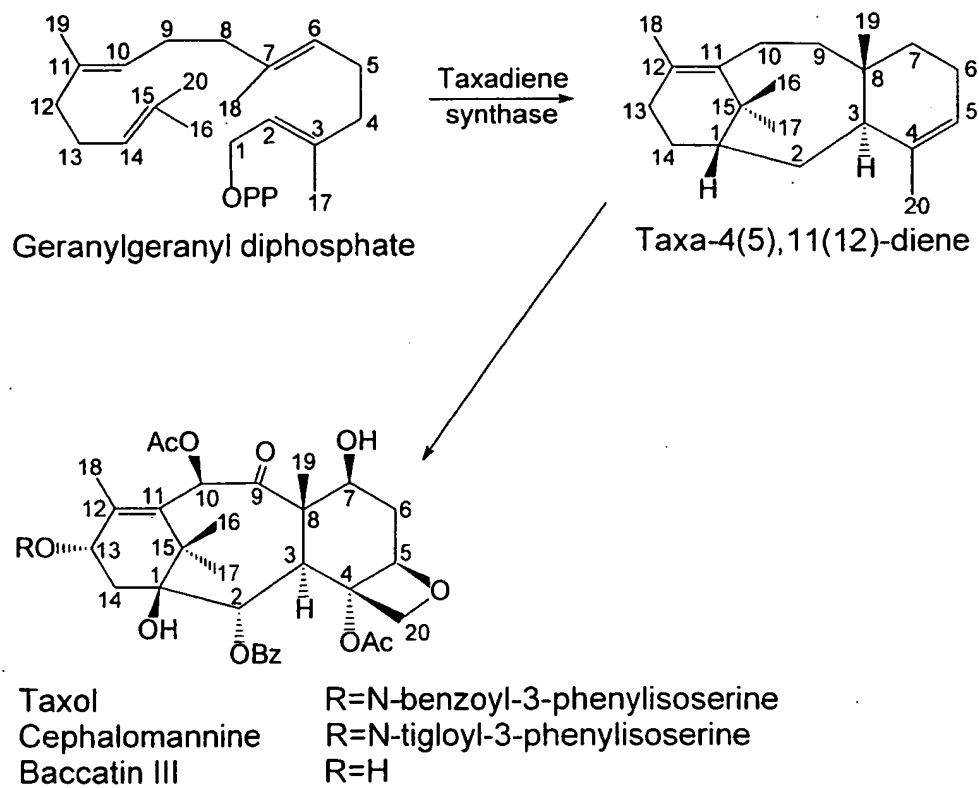


Fig. 1

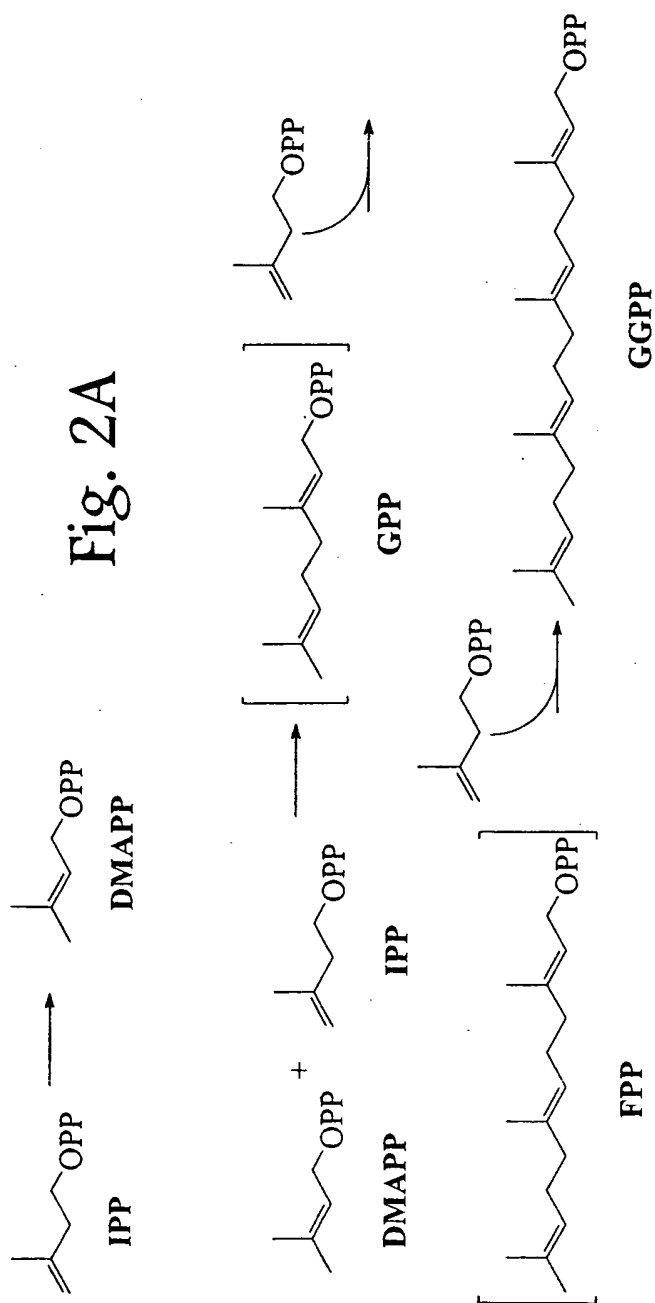
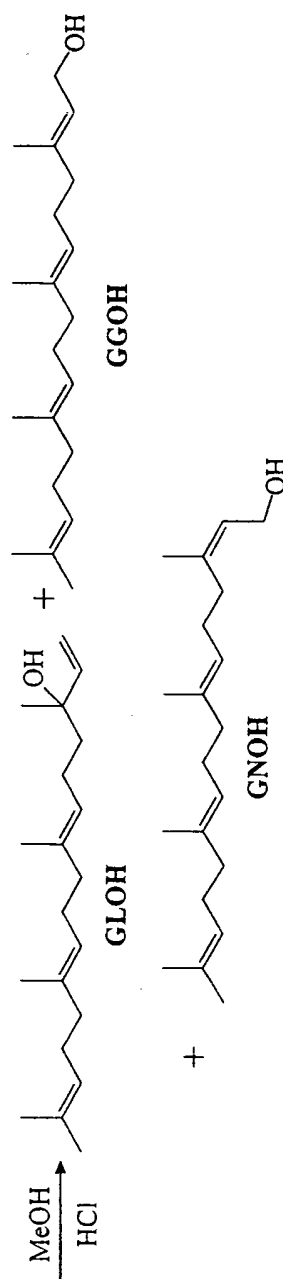


Fig. 2B



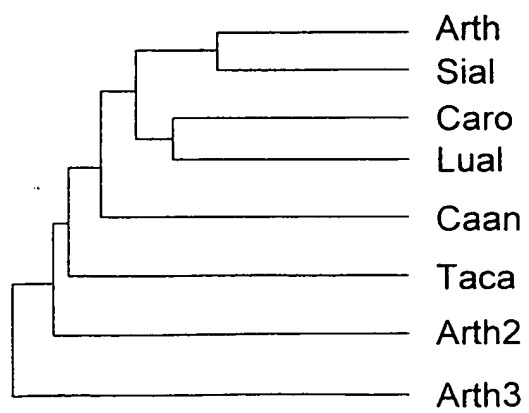


Fig. 3

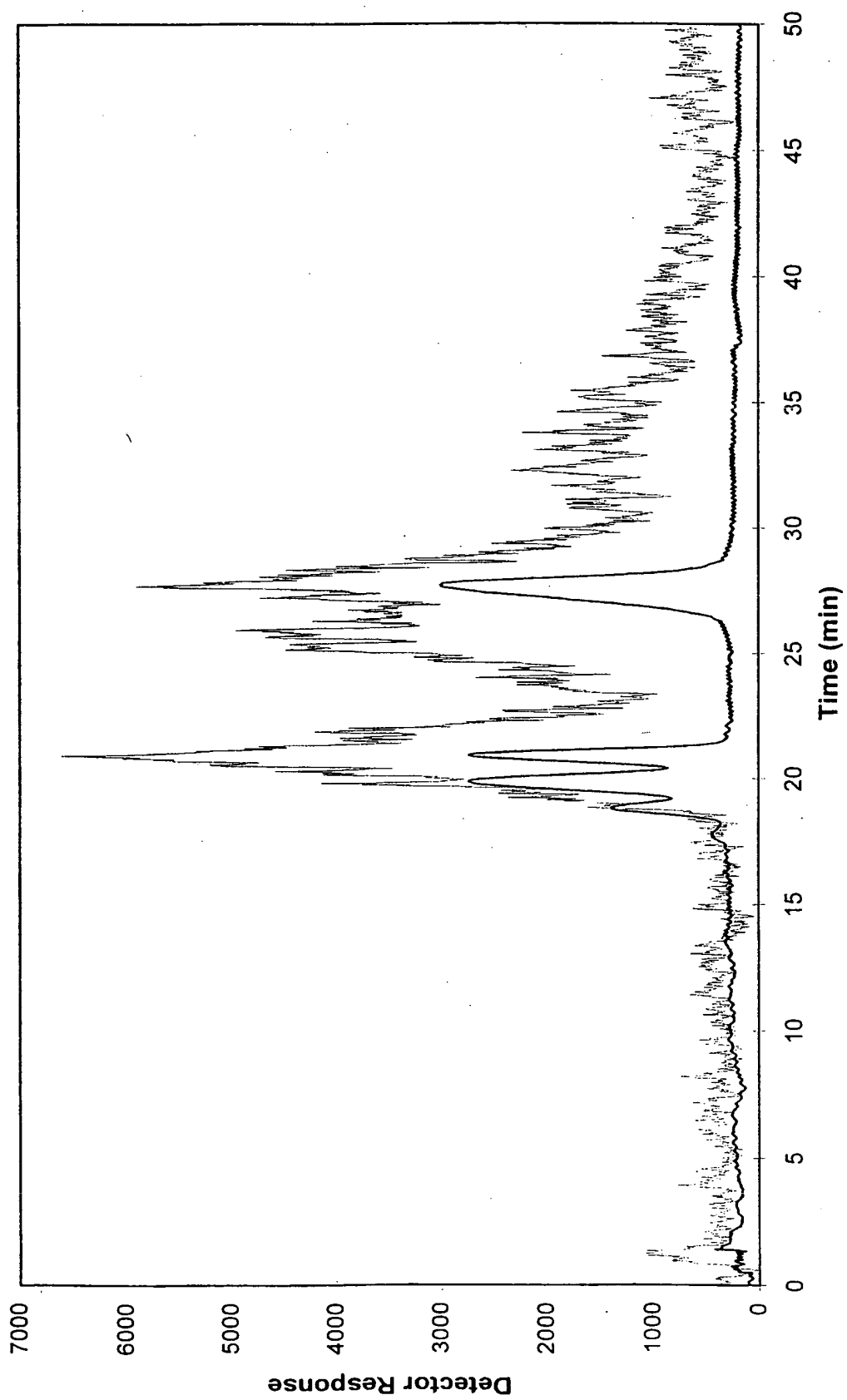


Fig. 4

GGPP Synthase and Taxadiene Synthase Activity After Methyl Jasmonate Induction

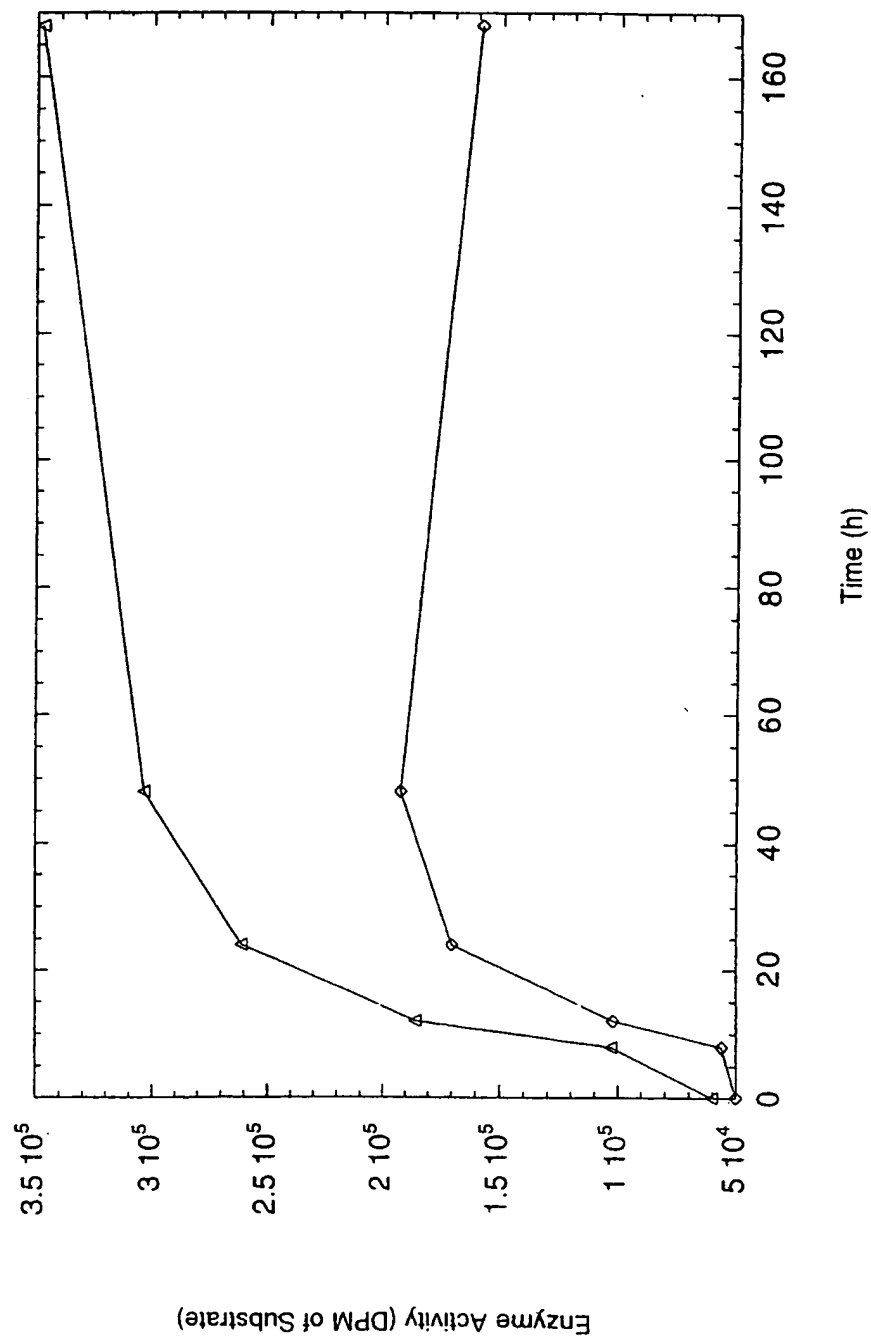


Fig. 5

SEQUENCE LISTING

<110> Croteau, Rodney B
Hefner, Jerry

<120> Nucleic Acids Encoding Taxus Geranylgeranyl Diphosphate
Synthase, And Methods of Use

<130> WSUR12423

<140>

<141>

<160> 34

<170> PatentIn Ver. 2.0

<210> 1

<211> 1889

<212> DNA

<213> Taxus canadensis

<220>

<221> CDS

<222> (308)..(1486)

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aggttttctg gaaggtgtgt gtgaaaattt gaagaaaatt aacaagactg taagtgtttt 120

tatatattta tgagcttttg tttacttggg tgttactgaa ttggaacata cgtgcatgtc 180

ggagcaaagc agcatatttg aaatttgttg gtgttctttg aggtgtgttg cggatataga 240

tttgattggt cagagttagt gtattttttt tttttgttgg ttagattaat tgggcaagtt 300

atagaga atg gct tac acg gca atg gca gca ggg acc caa agc ttg caa 349
Met Ala Tyr Thr Ala Met Ala Ala Gly Thr Gln Ser Leu Gln
1 5 10

ctc cgc act gtt gct tcc tat caa gaa tgc aat agt atg agg agt tgt 397
Leu Arg Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys
15 20 25 30

ttt aaa ttg aca cct ttt aaa agt ttt cat gga gtg aat ttc aat gtt 445
Phe Lys Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val
35 40 45

ccc tca ctg ggt gct gct aat tgt gag att atg ggt cac ctg aaa ctt 493
Pro Ser Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu
50 55 60

ggg tca ttg cca tat aaa caa tgt tcg gtg tca tct aaa tcc aca aaa 541
Gly Ser Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys
65 70 75

aca atg gcc cag ttg gtt gat ttg gct gaa aca gag aag gcg gag gga 589
Thr Met Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly
80 85 90

aag gat att gaa ttt gat ttc aac gag tat atg aag tcc aag gct gtg 637
Lys Asp Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val
95 100 105 110

gca gtg gat gcg gca ctg gat aag gca atc cca ctt gaa tat cct gaa	685
Ala Val Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu	
115 120 125	
aaa ata cat gaa tca atg agg tat tca ctt cta gca gga ggt aag cgc	733
Lys Ile His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg	
130 135 140	
gtc agg cct gct ctg tgc att gca gca tgt gag ctt gta gga ggg agt	781
Val Arg Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser	
145 150 155	
cag gac ctt gcc atg cca act gcc tgt gca atg gag atg att cat acc	829
Gln Asp Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr	
160 165 170	
atg tct ctg att cat gat gac ttg ccg tgc atg gat aat gat gat ttc	877
Met Ser Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe	
175 180 185 190	
aga aga ggg aag cca aca aat cac aag gtc ttt gga gag gac act gct	925
Arg Arg Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala	
195 200 205	
gtt ctt gca ggg gac gcc ctg ctt tca ttt gca ttt gag cat att gct	973
Val Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala	
210 215 220	
gtg gct aca agc aag act gtg cct agt gat agg act tta agg gtg ata	1021
Val Ala Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile	
225 230 235	
tct gaa ttg ggt aag aca ata ggc tct caa ggg ctt gta ggg ggg cag	1069
Ser Glu Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln	
240 245 250	
gtg gtt gat att aca tcc gag ggg gat gct aat gtg gac ctg aaa acc	1117
Val Val Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr	
255 260 265 270	
ctg gaa tgg att cat ata cac aag act gct gtg ctc ttg gaa tgt tca	1165
Leu Glu Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser	
275 280 285	
gtt gtg agt gga ggg atc ctt ggt ggt gct aca gag gac gag att gcg	1213
Val Val Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala	
290 295 300	
aga att cgg cgg tac gcc cgg tgt gtg ggg ctt ctg ttt cag gtt gtg	1261
Arg Ile Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val	
305 310 315	
gat gac ata ctt gat gtc act aaa tct tct gaa gaa ttg gga aag act	1309
Asp Asp Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr	
320 325 330	
gca gga aag gat ttg ctt act gat aag gct act tat ccc aag ttg atg	1357
Ala Gly Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met	
335 340 345 350	
ggc ctg gag aaa gca aaa gaa ttt gcc gct gaa ttg gcg acg aga gcc	1405
Gly Leu Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala	
355 360 365	

aag gaa gag ctg tca tcc ttt gat cag ata aag gct gca cct ttg ttg 1453
 Lys Glu Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu
 370 375 380

ggt ctt gca gat tac att gca ttc agg caa aac tgagaacaaa gctgtaaagc 1506
 Gly Leu Ala Asp Tyr Ile Ala Phe Arg Gln Asn
 385 390

tattcttaca tatcatctgt ttttttttga catctgctga aaattagcaa ataacttttt 1566
 caagtttgta tctccctga atcataacga ttcaggacat gaggtttctg gtaccattga 1626
 aaagggggcg ctcatgttag ttgtttttta gctaattcca acctgttttc tatgtttcca 1686
 ctttgatca attgatgta gattatgttt gtagggtga cattgttaga cttgtttacat 1746
 gtcataaat tgttttttgc ggccttaaca tggttttaac ttttactag caataagggtg 1806
 gcctaaagtg tttatgtaat ttttcaatat agatagatat cttttaacaa aaaaaaaaaa 1866
 aaaaaaaaaa aaaaaaaaaa aaa 1889

<210> 2
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 <212> PRT
 <213> *Taxus canadensis*

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 20 25 30
 Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
 35 40 45
 Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser
 50 55 60
 Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met
 65 70 75 80
 Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp
 85 90 95
 Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val
 100 105 110
 Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile
 115 120 125
 His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
 130 135 140
 Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp
 145 150 155 160
 Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser
 165 170 175
 Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg

180						185						190					
Gly	Lys	Pro 195	Thr	Asn	His	Lys	Val 200	Phe	Gly	Glu	Asp	Thr 205	Ala	Val	Leu		
Ala	Gly 210	Asp	Ala	Leu	Leu	Ser 215	Phe	Ala	Phe	Glu	His 220	Ile	Ala	Val	Ala		
Thr 225	Ser	Lys	Thr	Val	Pro 230	Ser	Asp	Arg	Thr	Leu 235	Arg	Val	Ile	Ser	Glu 240		
Leu	Gly	Lys	Thr	Ile 245	Gly	Ser	Gln	Gly	Leu 250	Val	Gly	Gly	Gln	Val 255	Val		
Asp	Ile	Thr	Ser 260	Glu	Gly	Asp	Ala	Asn 265	Val	Asp	Leu	Lys	Thr 270	Leu	Glu		
Trp	Ile	His 275	Ile	His	Lys	Thr	Ala 280	Val	Leu	Leu	Glu	Cys 285	Ser	Val	Val		
Ser	Gly 290	Gly	Ile	Leu	Gly	Gly 295	Ala	Thr	Glu	Asp	Glu 300	Ile	Ala	Arg	Ile		
Arg 305	Arg	Tyr	Ala	Arg	Cys 310	Val	Gly	Leu	Leu	Phe 315	Gln	Val	Val	Asp	Asp 320		
Ile	Leu	Asp	Val	Thr 325	Lys	Ser	Ser	Glu	Glu 330	Leu	Gly	Lys	Thr	Ala 335	Gly		
Lys	Asp	Leu	Leu 340	Thr	Asp	Lys	Ala	Thr 345	Tyr	Pro	Lys	Leu	Met 350	Gly	Leu		
Glu	Lys	Ala 355	Lys	Glu	Phe	Ala	Ala 360	Glu	Leu	Ala	Thr	Arg 365	Ala	Lys	Glu		
Glu	Leu	Ser 370	Ser	Phe	Asp	Gln 375	Ile	Lys	Ala	Ala	Pro 380	Leu	Leu	Gly	Leu		
Ala 385	Asp	Tyr	Ile	Ala	Phe 390	Arg	Gln	Asn									

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: reverse
degenerate primer

<220>

<221> misc difference

 $\langle 222 \rangle \quad (1) \cdot (20)$

<223> degenerate reverse PCR primer wherein "n" at position 9 represents I and "n" at positions 15 and 18 represent I, c or a

<400> 3

ttytayccnt tygc:ggnmq

20

<210> 4

<211> 861

<212> DNA

<213> *Taxus canadensis*

<400> 4

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ggttttctgc accgaaatcc tttaatttta aggtttcttg gaaggtgtgt gtgaaaattt 60
gaagaaaatt aacaagactg taagtgtttt tatatatatta tgagcttttg tttacttggg 120
tgttactgaa ttggaacata cgtgcatgtc ggagcaaagc agcatatttg aaatttgttg 180
gtgttctttg aggtgtgttg cggatataga tttgattgtt cagagttagt gtattttttt 240
tttttgttgg ttagattaat tgggcaagtt atagagaatg gcttacacgg caatggcagc 300
agggacccaa agcttgcaac tccgcactgt tgcttcctat caagaatgca atagtatgag 360
gagttgtttt aaattgacac cttttaaaag ttttcatgga gtgaatttca atgttccttc 420
actgggtgct gctaattgtg agattatggg tcacctgaaa cttgggtcat tgccatataa 480
acaatgttcg gtgtcatcta aatccacaaa aacaatggcc cagttggttg atttggctga 540
aacagagaag gcggagggaa aggatattga atttgatttc aacgagtata tgaagtccaa 600
ggctgtggca gtggatcggg cactggataa ggcaatccca cttgaatata ctgaaaaaat 660
acatgaatca atgaggtatt cacttctagc aggaggtaag cgcgtcaggc ctgctctgtg 720
cattgcagca tgtgagcttg taggaggagg tcaggacctt gccatgccaa ctgcctgtgc 780
aatggagatg attcatacca tgtctctgat tcatgatgac ttgccgtgca tggataatga 840
tgatttcaga agagggaagc c 861
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<210> 5

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: forward
degenerate primer

<220>

<221> misc_difference

<222> (1)..(22)

<223> degenerate PCR primer

<400> 5

tggcttacac ggcaatggca gc

22

<210> 6

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: non-degenerate
reverse PCR primer

<220>

<221> misc_difference

<222> (1)..(23)
<223> Non-degenerate PCR primer

<400> 6
ggcttaccac agccgaaatc atc

23

<210> 7
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<221> misc_difference
<222> (1)..(38)
<223> PCR primer containing KpnI site

<400> 7
gggttacctc agttttgcct gaatgcaatg taatctgc

38

<210> 8
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<220>
<221> misc_difference
<222> (1)..(35)
<223> PCR primer including BamHI site

<400> 8
gaagatctat ggcttacacg gcaatggcag caggg

35

<210> 9
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<220>
<221> misc_difference
<222> (1)..(43)
<223> PCR primer for synthesizing Tr295 truncation product

<400> 9
gaagatctat gtttgatttc aacgagtata tgaagtccaa ggc

43

<210> 10
<211> 38
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<220>

<221> misc_difference

<222> (1)..(38)

<223> PCR primer for synthesizing Tr313 truncation

<400> 10

gaagatctat gaagtccaag gctgtggcag tggatgcg

38

<210> 11

<211> 885

<212> DNA

<213> Taxus cuspidata

<220>

<221> CDS

<222> (1)..(855)

<400> 11

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Phe	Asp	Phe	Asn	Glu	Tyr	Met	Lys	Ser	Lys	Ala	Val	Ala	Val	Asp	Ala	
1				5					10					15		

gca	ctg	gat	aag	gca	atc	cca	ctt	gaa	tat	cct	gaa	aaa	ata	cat	gaa	96
Ala	Leu	Asp	Lys	Ala	Ile	Pro	Leu	Glu	Tyr	Pro	Glu	Lys	Ile	His	Glu	
			20					25					30			

tca	atg	agg	tat	tca	ctt	cta	gca	gga	ggg	aag	cgc	gtt	agg	cct	gct	144
Ser	Met	Arg	Tyr	Ser	Leu	Leu	Ala	Gly	Gly	Lys	Arg	Val	Arg	Pro	Ala	
		35					40					45				

ctg	tgc	att	gca	gca	tgt	gag	ctt	gta	gga	ggg	agt	cag	gac	ctt	gcc	192
Leu	Cys	Ile	Ala	Ala	Cys	Glu	Leu	Val	Gly	Gly	Ser	Gln	Asp	Leu	Ala	
	50					55					60					

atg	cca	act	gcc	tgt	gca	atg	gag	atg	att	cat	acc	atg	tct	ctg	att	240
Met	Pro	Thr	Ala	Cys	Ala	Met	Glu	Met	Ile	His	Thr	Met	Ser	Leu	Ile	
	65				70					75					80	

cat	gat	gac	ttg	ccc	tgc	atg	gat	aat	gat	gat	ttc	aga	aga	ggg	aag	288
His	Asp	Asp	Leu	Pro	Cys	Met	Asp	Asn	Asp	Asp	Phe	Arg	Arg	Gly	Lys	
			85					90						95		

ccc	aca	aat	cac	aag	gtc	ttt	gga	gag	gac	act	gct	gtt	ctt	gca	ggg	336
Pro	Thr	Asn	His	Lys	Val	Phe	Gly	Glu	Asp	Thr	Ala	Val	Leu	Ala	Gly	
			100					105					110			

gat	gcc	ctg	ctt	tca	ttt	gca	ttt	gag	cat	att	gct	gtg	gct	aca	agc	384
Asp	Ala	Leu	Leu	Ser	Phe	Ala	Phe	Glu	His	Ile	Ala	Val	Ala	Thr	Ser	
		115					120					125				

aag	act	gtg	cct	agt	gat	agg	act	tta	agg	gtg	ata	tct	gaa	ttg	ggg	432
Lys	Thr	Val	Pro	Ser	Asp	Arg	Thr	Leu	Arg	Val	Ile	Ser	Glu	Leu	Gly	
	130					135					140					

aag	aca	ata	ggc	tct	caa	ggg	ctt	gta	ggg	gga	cag	gtg	gtt	gat	att	480
Lys	Thr	Ile	Gly	Ser	Gln	Gly	Leu	Val	Gly	Gly	Gln	Val	Val	Asp	Ile	
	145				150				155					160		

aca	tcc	gag	ggg	gat	gct	aat	gtg	gac	ctg	aaa	acc	ctg	gaa	tgg	att	528
Thr	Ser	Glu	Gly	Asp	Ala	Asn	Val	Asp	Leu	Lys	Thr	Leu	Glu	Trp	Ile	

165										170					175					
cat	ata	cac	aag	act	gct	gtg	ctc	ttg	gaa	tgt	tca	gtt	gtg	agt	gga	576				
His	Ile	His	Lys	Thr	Ala	Val	Leu	Leu	Glu	Cys	Ser	Val	Val	Ser	Gly					
			180					185					190							
ggg	atc	ctt	ggt	ggt	gct	aca	gag	gat	gag	att	gcg	aga	att	cgg	cgg	624				
Gly	Ile	Leu	Gly	Gly	Ala	Thr	Glu	Asp	Glu	Ile	Ala	Arg	Ile	Arg	Arg					
		195					200				205									
tat	gcc	cgg	tgt	gtg	ggg	ctt	ctg	ttt	cag	gtt	gtt	gat	gac	ata	ctt	672				
Tyr	Ala	Arg	Cys	Val	Gly	Leu	Leu	Phe	Gln	Val	Val	Asp	Asp	Ile	Leu					
	210					215					220									
gat	gtc	act	aaa	tct	tct	gaa	gaa	ttg	gga	aag	act	gca	ggg	aag	gat	720				
Asp	Val	Thr	Lys	Ser	Ser	Glu	Glu	Leu	Gly	Lys	Thr	Ala	Gly	Lys	Asp					
225					230					235					240					
ttg	cta	act	gat	aag	gct	act	tat	ccc	aag	ttg	atg	ggc	ctg	gag	aaa	768				
Leu	Leu	Thr	Asp	Lys	Ala	Thr	Tyr	Pro	Lys	Leu	Met	Gly	Leu	Glu	Lys					
				245					250					255						
gca	aaa	gaa	ttt	gct	gct	gaa	ttg	gcg	acg	aga	gcc	aag	gaa	gag	ctg	816				
Ala	Lys	Glu	Phe	Ala	Ala	Glu	Leu	Ala	Thr	Arg	Ala	Lys	Glu	Glu	Leu					
			260					265					270							
tca	tcc	ttt	gat	cag	ata	aag	gct	gca	cct	tta	ttg	ggg	cttgcagatt			865				
Ser	Ser	Phe	Asp	Gln	Ile	Lys	Ala	Ala	Pro	Leu	Leu	Gly								
		275					280					285								
acattgcatt	caggcaaaac															885				

<210> 12

<211> 285

<212> PRT

<213> Taxus cuspidata

<400> 12

Phe	Asp	Phe	Asn	Glu	Tyr	Met	Lys	Ser	Lys	Ala	Val	Ala	Val	Asp	Ala
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Ala	Leu	Asp	Lys	Ala	Ile	Pro	Leu	Glu	Tyr	Pro	Glu	Lys	Ile	His	Glu
			20					25					30		

Ser	Met	Arg	Tyr	Ser	Leu	Leu	Ala	Gly	Gly	Lys	Arg	Val	Arg	Pro	Ala
		35					40					45			

Leu	Cys	Ile	Ala	Ala	Cys	Glu	Leu	Val	Gly	Gly	Ser	Gln	Asp	Leu	Ala
	50					55					60				

Met	Pro	Thr	Ala	Cys	Ala	Met	Glu	Met	Ile	His	Thr	Met	Ser	Leu	Ile
65					70					75					80

His	Asp	Asp	Leu	Pro	Cys	Met	Asp	Asn	Asp	Asp	Phe	Arg	Arg	Gly	Lys
				85					90					95	

Pro	Thr	Asn	His	Lys	Val	Phe	Gly	Glu	Asp	Thr	Ala	Val	Leu	Ala	Gly
			100					105					110		

Asp	Ala	Leu	Leu	Ser	Phe	Ala	Phe	Glu	His	Ile	Ala	Val	Ala	Thr	Ser
		115					120					125			

Lys	Thr	Val	Pro	Ser	Asp	Arg	Thr	Leu	Arg	Val	Ile	Ser	Glu	Leu	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

130 135 140
 Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val Asp Ile
 145 150 155 160
 Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu Trp Ile
 165 170 175
 His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val Ser Gly
 180 185 190
 Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile Arg Arg
 195 200 205
 Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp Ile Leu
 210 215 220
 Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly Lys Asp
 225 230 235 240
 Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu Glu Lys
 245 250 255
 Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu Glu Leu
 260 265 270
 Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly
 275 280 285

<210> 13
 <211> 1179
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: nucleic acid
 encoding Taxus GGPP synthase protein

<220>
 <221> CDS
 <222> (1)..(1179)
 <223> computer-generated nucleic acid sequence encoding
 a Taxus GGPP synthase protein

<400> 13
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 Met Gly Tyr Thr Ala Met Ala Ala Gly Thr Gln Ser Leu Gln Leu Arg
 1 5 10 15
 act gtt gct tcc tat caa gaa tgc aat agt atg agg agt tgt ttt aaa 96
 Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys
 20 25 30
 ttg aca cct ttt aaa agt ttt cat gga gtg aat ttc aat gtt ccc tca 144
 Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
 35 40 45
 ctg ggt gct gct aat tgt gag att atg ggt cac ctg aaa ctt ggg tca 192
 Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser
 50 55 60
 ttg cca tat aaa caa tgt tcg gtg tca tct aaa tcc aca aaa aca atg 240
 Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met

65	70	75	80	
gcc cag ttg gtt gat ttg gct gaa aca gag aag gcg gag gga aag gat				288
Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp	85	90	95	
att gaa ttt gat ttc aac gag tat atg aag tcc aag gct gtg gca gtg				336
Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val	100	105	110	
gat gcg gca ctg gat aag gca atc cca ctt gaa tat cct gaa aaa ata				384
Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile	115	120	125	
cat gaa tca atg agg tat tca ctt cta gca gga ggt aag cgc gtc agg				432
His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg	130	135	140	
cct gct ctg tgc att gca gca tgt gag ctt gta gga ggg agt cag gac				480
Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp	145	150	155	160
ctt gcc atg cca act gcc tgt gca atg gag atg att cat acc atg tct				528
Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser	165	170	175	
ctg att cat gat gac ttg ccg tgc atg gat aat gat gat ttc aga aga				576
Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg	180	185	190	
ggg aag cca aca aat cac aag gtc ttt gga gag gac act gct gtt ctt				624
Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu	195	200	205	
gca ggg gac gcc ctg ctt tca ttt gca ttt gag cat att gct gtg gct				672
Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala	210	215	220	
aca agc aag act gtg cct agt gat agg act tta agg gtg ata tct gaa				720
Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu	225	230	235	240
ttg ggt aag aca ata ggc tct caa ggg ctt gta ggg ggg cag gtg gtt				768
Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val	245	250	255	
gat att aca tcc gag ggg gat gct aat gtg gac ctg aaa acc ctg gaa				816
Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu	260	265	270	
tgg att cat ata cac aag act gct gtg ctc ttg gaa tgt tca gtt gtg				864
Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val	275	280	285	
agt gga ggg atc ctt ggt ggt gct aca gag gac gag att gcg aga att				912
Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile	290	295	300	
cgg cgg tac gcc cgg tgt gtg ggg ctt ctg ttt cag gtt gtg gat gac				960
Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp	305	310	315	320
ata ctt gat gtc act aaa tct tct gaa gaa ttg gga aag act gca gga				1008
Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly				

325	330	335	
aag gat ttg ctt act gat aag gct act tat ccc aag ttg atg ggc ctg			1056
Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu			
340	345	350	
gag aaa gca aaa gaa ttt gcc gct gaa ttg gcg acg aga gcc aag gaa			1104
Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu			
355	360	365	
gag ctg tca tcc ttt gat cag ata aag gct gca cct ttg ttg ggt ctt			1152
Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu			
370	375	380	
gca gat tac att gca ttc agg caa aac			1179
Ala Asp Tyr Ile Ala Phe Arg Gln Asn			
385	390		

<210> 14

<211> 393

<212> PRT

<213> Artificial Sequence

<400> 14

Met Gly Tyr Thr Ala Met Ala Ala Gly Thr Gln Ser Leu Gln Leu Arg			
1	5	10	15
Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys			
20	25	30	
Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser			
35	40	45	
Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser			
50	55	60	
Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met			
65	70	75	80
Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp			
85	90	95	
Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val			
100	105	110	
Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile			
115	120	125	
His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg			
130	135	140	
Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp			
145	150	155	160
Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser			
165	170	175	
Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg			
180	185	190	
Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu			
195	200	205	

Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala
 210 215 220

Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu
 225 230 235 240

Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
 245 250 255

Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu
 260 265 270

Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
 275 280 285

Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
 290 295 300

Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
 305 310 315 320

Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
 325 330 335

Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350

Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
 355 360 365

Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380

Ala Asp Tyr Ile Ala Phe Arg Gln Asn
 385 390

<210> 15
 <211> 1179
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: nucleic acid
 sequence encoding Taxus GGPP synthase

<220>
 <221> CDS
 <222> (1)..(1179)
 <223> Computer-generated nucleic acid sequence encoding
 Taxus GGPP synthase protein

<400> 15
 atg gct tac acg gga atg gca gca ggg acc caa agc ttg caa ctc cgc 48
 Met Ala Tyr Thr Gly Met Ala Ala Gly Thr Gln Ser Leu Gln Leu Arg
 1 5 10 15

act gtt gct tcc tat caa gaa tgc aat agt atg agg agt tgt ttt aaa 96
 Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys
 20 25 30

ttg aca cct ttt aaa agt ttt cat gga gtg aat ttc aat gtt ccc tca 144
 Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
 35 40 45

ctg ggt gct gct aat tgt gag att atg ggt cac ctg aaa ctt ggg tca	192
Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser	
50 55 60	
ttg cca tat aaa caa tgt tgc gtg tca tct aaa tcc aca aaa aca atg	240
Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met	
65 70 75 80	
gcc cag ttg gtt gat ttg gct gaa aca gag aag gcg gag gga aag gat	288
Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp	
85 90 95	
att gaa ttt gat ttc aac gag tat atg aag tcc aag gct gtg gca gtg	336
Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val	
100 105 110	
gat gcg gca ctg gat aag gca atc cca ctt gaa tat cct gaa aaa ata	384
Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile	
115 120 125	
cat gaa tca atg agg tat tca ctt cta gca gga ggt aag cgc gtc agg	432
His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg	
130 135 140	
cct gct ctg tgc att gca gca tgt gag ctt gta gga ggg agt cag gac	480
Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp	
145 150 155 160	
ctt gcc atg cca act gcc tgt gca atg gag atg att cat acc atg tct	528
Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser	
165 170 175	
ctg att cat gat gac ttg ccg tgc atg gat aat gat gat ttc aga aga	576
Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg	
180 185 190	
ggg aag cca aca aat cac aag gtc ttt gga gag gac act gct gtt ctt	624
Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu	
195 200 205	
gca ggg gac gcc ctg ctt tca ttt gca ttt gag cat att gct gtg gct	672
Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala	
210 215 220	
aca agc aag act gtg cct agt gat agg act tta agg gtg ata tct gaa	720
Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu	
225 230 235 240	
ttg ggt aag aca ata ggc tct caa ggg ctt gta ggg ggg cag gtg gtt	768
Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val	
245 250 255	
gat att aca tcc gag ggg gat gct aat gtg gac ctg aaa acc ctg gaa	816
Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu	
260 265 270	
tgg att cat ata cac aag act gct gtg ctc ttg gaa tgt tca gtt gtg	864
Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val	
275 280 285	
agt gga ggg atc ctt ggt ggt gct aca gag gac gag att gcg aga att	912
Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile	
290 295 300	

cgg cgg tac gcc cgg tgt gtg ggg ctt ctg ttt cag gtt gtg gat gac 960
 Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp 320
 305 310 315
 ata ctt gat gtc act aaa tct tct gaa gaa ttg gga aag act gca gga 1008
 Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly 335
 325 330
 aag gat ttg ctt act gat aag gct act tat ccc aag ttg atg ggc ctg 1056
 Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu 350
 340 345
 gag aaa gca aaa gaa ttt gcc gct gaa ttg gcg acg aga gcc aag gaa 1104
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu 365
 355 360
 gag ctg tca tcc ttt gat cag ata aag gct gca cct ttg ttg ggt ctt 1152
 Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu 380
 370 375
 gca gat tac att gca ttc agg caa aac 1179
 Ala Asp Tyr Ile Ala Phe Arg Gln Asn 390
 385 390

<210> 16

<211> 393

<212> PRT

<213> Artificial Sequence

<400> 16

Met Ala Tyr Thr Gly Met Ala Ala Gly Thr Gln Ser Leu Gln Leu Arg 15
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 Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys 30
 20 25 30
 Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser 45
 35 40 45
 Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser 60
 50 55 60
 Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met 80
 65 70 75 80
 Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp 95
 85 90 95
 Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val 110
 100- 105 110
 Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile 125
 115 120 125
 His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg 140
 130 135 140
 Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp 160
 145 150 155 160
 Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser 175
 165 170 175

Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg
 180 185 190
 Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu
 195 200 205
 Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala
 210 215 220
 Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu
 225 230 235 240
 Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
 245 250 255
 Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu
 260 265 270
 Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
 275 280 285
 Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
 290 295 300
 Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
 305 310 315 320
 Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
 325 330 335
 Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
 355 360 365
 Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380
 Ala Asp Tyr Ile Ala Phe Arg Gln Asn
 385 390

<210> 17

<211> 1179

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: nucleic acid
sequence encoding Taxus GGPP synthase

<220>

<221> CDS

<222> (1)..(1179)

<223> Computer-generated nucleic acid sequence encoding
Taxus GGPP synthase protein

<400> 17

atg gct tac acg gca atg gga gca ggg acc caa agc ttg caa ctc cgc 48
 Met Ala Tyr Thr Ala Met Gly Ala Gly Thr Gln Ser Leu Gln Leu Arg
 1 5 10 15

act gtt gct tcc tat caa gaa tgc aat agt atg agg agt tgt ttt aaa	96
Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys	
20 25 30	
ttg aca cct ttt aaa agt ttt cat gga gtg aat ttc aat gtt ccc tca	144
Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser	
35 40 45	
ctg ggt gct gct aat tgt gag att atg ggt cac ctg aaa ctt ggg tca	192
Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser	
50 55 60	
ttg cca tat aaa caa tgt tgc gtg tca tct aaa tcc aca aaa aca atg	240
Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met	
65 70 75 80	
gcc cag ttg gtt gat ttg gct gaa aca gag aag gcg gag gga aag gat	288
Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp	
85 90 95	
att gaa ttt gat ttc aac gag tat atg aag tcc aag gct gtg gca gtg	336
Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val	
100 105 110	
gat gcg gca ctg gat aag gca atc cca ctt gaa tat cct gaa aaa ata	384
Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile	
115 120 125	
cat gaa tca atg agg tat tca ctt cta gca gga ggt aag cgc gtc agg	432
His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg	
130 135 140	
cct gct ctg tgc att gca gca tgt gag ctt gta gga ggg agt cag gac	480
Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp	
145 150 155 160	
ctt gcc atg cca act gcc tgt gca atg gag atg att cat acc atg tct	528
Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser	
165 170 175	
ctg att cat gat gac ttg ccg tgc atg gat aat gat gat ttc aga aga	576
Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg	
180 185 190	
ggg aag cca aca aat cac aag gtc ttt gga gag gac act gct gtt ctt	624
Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu	
195 200 205	
gca ggg gac gcc ctg ctt tca ttt gca ttt gag cat att gct gtg gct	672
Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala	
210 215 220	
aca agc aag act gtg cct agt gat agg act tta agg gtg ata tct gaa	720
Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu	
225 230 235 240	
ttg ggt aag aca ata ggc tct caa ggg ctt gta ggg ggg cag gtg gtt	768
Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val	
245 250 255	
gat att aca tcc gag ggg gat gct aat gtg gac ctg aaa acc ctg gaa	816
Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu	
260 265 270	

tgg att cat ata cac aag act gct gtg ctc ttg gaa tgt tca gtt gtg 864
 Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
 275 280 285
 agt gga ggg atc ctt ggt ggt gct aca gag gac gag att gcg aga att 912
 Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
 290 295 300
 cgg cgg tac gcc cgg tgt gtg ggg ctt ctg ttt cag gtt gtg gat gac 960
 Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
 305 310 315 320
 ata ctt gat gtc act aaa tct tct gaa gaa ttg gga aag act gca gga 1008
 Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
 325 330 335
 aag gat ttg ctt act gat aag gct act tat ccc aag ttg atg ggc ctg 1056
 Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350
 gag aaa gca aaa gaa ttt gcc gct gaa ttg gcg acg aga gcc aag gaa 1104
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
 355 360 365
 gag ctg tca tcc ttt gat cag ata aag gct gca cct ttg ttg ggt ctt 1152
 Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380
 gca gat tac att gca ttc agg caa aac 1179
 Ala Asp Tyr Ile Ala Phe Arg Gln Asn
 385 390

<210> 18

<211> 393

<212> PRT

<213> Artificial Sequence

<400> 18

Met Ala Tyr Thr Ala Met Gly Ala Gly Thr Gln Ser Leu Gln Leu Arg
 1 5 10 15
 Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys
 20 25 30
 Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
 35 40 45
 Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser
 50 55 60
 Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met
 65 70 75 80
 Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp
 85 90 95
 Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val
 100 105 110
 Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile
 115 120 125
 His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg

130	135	140
Pro Ala Leu Cys Ile 145	Ala Ala Cys Glu Leu Val 150	Gly Gly Ser Gln Asp 155 160
Leu Ala Met Pro Thr 165	Ala Cys Ala Met Glu Met 170	Ile His Thr Met Ser 175
Leu Ile His Asp Asp 180	Leu Pro Cys Met Asp Asn 185	Asp Asp Phe Arg Arg 190
Gly Lys Pro Thr Asn His 195	Lys Val Phe Gly Glu Asp 200	Thr Ala Val Leu 205
Ala Gly Asp Ala Leu Leu 210	Ser Phe Ala Phe Glu His 215 220	Ile Ala Val Ala
Thr Ser Lys Thr Val Pro 225	Ser Asp Arg Thr Leu Arg 230 235	Val Ile Ser Glu 240
Leu Gly Lys Thr Ile Gly 245	Ser Gln Gly Leu Val Gly 250	Gly Gln Val Val 255
Asp Ile Thr Ser Glu Gly 260	Asp Ala Asn Val Asp Leu 265	Lys Thr Leu Glu 270
Trp Ile His Ile His Lys 275	Thr Ala Val Leu Leu Glu 280	Cys Ser Val Val 285
Ser Gly Gly Ile Leu Gly 290	Gly Ala Thr Glu Asp Glu 295 300	Ile Ala Arg Ile
Arg Arg Tyr Ala Arg Cys 305	Val Gly Leu Leu Phe Gln 310 315	Val Val Asp Asp 320
Ile Leu Asp Val Thr Lys 325	Ser Ser Glu Glu Leu Gly 330	Lys Thr Ala Gly 335
Lys Asp Leu Leu Thr Asp 340	Lys Ala Thr Tyr Pro Lys 345	Leu Met Gly Leu 350
Glu Lys Ala Lys Glu Phe 355	Ala Ala Glu Leu Ala Thr 360	Arg Ala Lys Glu 365
Glu Leu Ser Ser Phe Asp 370	Gln Ile Lys Ala Ala Pro 375 380	Leu Leu Gly Leu
Ala Asp Tyr Ile Ala Phe 385	Arg Gln Asn	

<210> 19

<211> 1179

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: nucleic acid
sequence encoding Taxus GGPP synthase

<220>

<221> CDS

<222> (1)..(1179)

<223> Computer-generated nucleic acid sequence encoding

Taxus GGPP synthase protein

<400> 19

atg gct tac acg gca atg gca gga ggg acc caa agc ttg caa ctc cgc	48
Met Ala Tyr Thr Ala Met Ala Gly Gly Thr Gln Ser Leu Gln Leu Arg	
1 5 10 15	
act gtt gct tcc tat caa gaa tgc aat agt atg agg agt tgt ttt aaa	96
Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys	
20 25 30	
ttg aca cct ttt aaa agt ttt cat gga gtg aat ttc aat gtt ccc tca	144
Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser	
35 40 45	
ctg ggt gct gct aat tgt gag att atg ggt cac ctg aaa ctt ggg tca	192
Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser	
50 55 60	
ttg cca tat aaa caa tgt tgc gtg tca tct aaa tcc aca aaa aca atg	240
Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met	
65 70 75 80	
gcc cag ttg gtt gat ttg gct gaa aca gag aag gcg gag gga aag gat	288
Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp	
85 90 95	
att gaa ttt gat ttc aac gag tat atg aag tcc aag gct gtg gca gtg	336
Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val	
100 105 110	
gat gcg gca ctg gat aag gca atc cca ctt gaa tat cct gaa aaa ata	384
Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile	
115 120 125	
cat gaa tca atg agg tat tca ctt cta gca gga ggt aag cgc gtc agg	432
His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg	
130 135 140	
cct gct ctg tgc att gca gca tgt gag ctt gta gga ggg agt cag gac	480
Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp	
145 150 155 160	
ctt gcc atg cca act gcc tgt gca atg gag atg att cat acc atg tct	528
Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser	
165 170 175	
ctg att cat gat gac ttg ccg tgc atg gat aat gat gat ttc aga aga	576
Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg	
180 185 190	
ggg aag cca aca aat cac aag gtc ttt gga gag gac act gct gtt ctt	624
Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu	
195 200 205	
gca ggg gac gcc ctg ctt tca ttt gca ttt gag cat att gct gtg gct	672
Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala	
210 215 220	
aca agc aag act gtg cct agt gat agg act tta agg gtg ata tct gaa	720
Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu	
225 230 235 240	
ttg ggt aag aca ata ggc tct caa ggg ctt gta ggg ggg cag gtg gtt	768

Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
 245 250 255
 gat att aca tcc gag ggg gat gct aat gtg gac ctg aaa acc ctg gaa 816
 Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu
 260 265 270
 tgg att cat ata cac aag act gct gtg ctc ttg gaa tgt tca gtt gtg 864
 Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
 275 280 285
 agt gga ggg atc ctt ggt ggt gct aca gag gac gag att gcg aga att 912
 Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
 290 295 300
 cgg cgg tac gcc cgg tgt gtg ggg ctt ctg ttt cag gtt gtg gat gac 960
 Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
 305 310 315 320
 ata ctt gat gtc act aaa tct tct gaa gaa ttg gga aag act gca gga 1008
 Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
 325 330 335
 aag gat ttg ctt act gat aag gct act tat ccc aag ttg atg ggc ctg 1056
 Lys Asp Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350
 gag aaa gca aaa gaa ttt gcc gct gaa ttg gcg acg aga gcc aag gaa 1104
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
 355 360 365
 gag ctg tca tcc ttt gat cag ata aag gct gca cct ttg ttg ggt ctt 1152
 Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380
 gca gat tac att gca ttc agg caa aac 1179
 Ala Asp Tyr Ile Ala Phe Arg Gln Asn
 385 390

<210> 20

<211> 393

<212> PRT

<213> Artificial Sequence

<400> 20

Met Ala Tyr Thr Ala Met Ala Gly Gly Thr Gln Ser Leu Gln Leu Arg
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 20 25 30
 Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
 35 40 45
 Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser
 50 55 60
 Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met
 65 70 75 80
 Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp
 85 90 95

Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val
 100 105 110
 Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile
 115 120 125
 His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
 130 135 140
 Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp
 145 150 155 160
 Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser
 165 170 175
 Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg
 180 185 190
 Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu
 195 200 205
 Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala
 210 215 220
 Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu
 225 230 235 240
 Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
 245 250 255
 Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu
 260 265 270
 Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
 275 280 285
 Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
 290 295 300
 Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
 305 310 315 320
 Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
 325 330 335
 Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
 355 360 365
 Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380
 Ala Asp Tyr Ile Ala Phe Arg Gln Asn
 385 390

<210> 21

<211> 1179

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: nucleic acid
sequence encoding Taxus GGPP synthase

<220>

<221> CDS

<222> (1)..(1179)

<223> Computer-generated nucleic acid sequence encoding
Taxus GGPP synthase protein

<400> 21

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Met Ala Tyr Thr Ala Met Ala Ala Thr Gln Ser Leu Gln Leu Arg	
1 5 10 15	
act gtt gct tcc tat caa gaa tgc aat agt atg agg agt tgt ttt aaa	96
Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys	
20 25 30	
ttg aca cct ttt aaa agt ttt cat gga gtg aat ttc aat gtt ccc tca	144
Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser	
35 40 45	
ctg ggt gct gct aat tgt gag att atg ggt cac ctg aaa ctt ggg tca	192
Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser	
50 55 60	
ttg cca tat aaa caa tgt tcg gtg tca tct aaa tcc aca aaa aca atg	240
Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met	
65 70 75 80	
gcc cag ttg gtt gat ttg gct gaa aca gag aag gcg gag gga aag gat	288
Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp	
85 90 95	
att gaa ttt gat ttc aac gag tat atg aag tcc aag gct gtg gca gtg	336
Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val	
100 105 110	
gat gcg gca ctg gat aag gca atc cca ctt gaa tat cct gaa aaa ata	384
Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile	
115 120 125	
cat gaa tca atg agg tat tca ctt cta gca gga ggt aag cgc gtc agg	432
His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg	
130 135 140	
cct gct ctg tgc att gca gca tgt gag ctt gta gga ggg agt cag gac	480
Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp	
145 150 155 160	
ctt gcc atg cca act gcc tgt gca atg gag atg att cat acc atg tct	528
Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser	
165 170 175	
ctg att cat gat gac ttg ccg tgc atg gat aat gat gat ttc aga aga	576
Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg	
180 185 190	
ggg aag cca aca aat cac aag gtc ttt gga gag gac act gct gtt ctt	624
Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu	
195 200 205	
gca ggg gac gcc ctg ctt tca ttt gca ttt gag cat att gct gtg gct	672
Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala	

210	215	220	
aca agc aag act gtg cct agt gat agg act tta agg gtg ata tct gaa			720
Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu			
225	230	235	240
ttg ggt aag aca ata ggc tct caa ggg ctt gta ggg ggg cag gtg gtt			768
Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val			
	245	250	255
gat att aca tcc gag ggg gat gct aat gtg gac ctg aaa acc ctg gaa			816
Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu			
	260	265	270
tgg att cat ata cac aag act gct gtg ctc ttg gaa tgt tca gtt gtg			864
Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val			
	275	280	285
agt gga ggg atc ctt ggt ggt gct aca gag gac gag att gcg aga att			912
Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile			
	290	295	300
cgg cgg tac gcc cgg tgt gtg ggg ctt ctg ttt cag gtt gtg gat gac			960
Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp			
	305	310	315
ata ctt gat gtc act aaa tct tct gaa gaa ttg gga aag act gca gga			1008
Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly			
	325	330	335
aag gat ttg ctt act gat aag gct act tat ccc aag ttg atg ggc ctg			1056
Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu			
	340	345	350
gag aaa gca aaa gaa ttt gcc gct gaa ttg gcg acg aga gcc aag gaa			1104
Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu			
	355	360	365
gag ctg tca tcc ttt gat cag ata aag gct gca cct ttg ttg ggt ctt			1152
Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu			
	370	375	380
gca gat tac att gca ttc agg caa aac			1179
Ala Asp Tyr Ile Ala Phe Arg Gln Asn			
	385	390	

<210> 22

<211> 393

<212> PRT

<213> Artificial Sequence

<400> 22

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Thr	Val	Ala	Ser	Tyr	Gln	Glu	Cys	Asn	Ser	Met	Arg	Ser	Cys	Phe	Lys
		20						25					30		

Leu	Thr	Pro	Phe	Lys	Ser	Phe	His	Gly	Val	Asn	Phe	Asn	Val	Pro	Ser
		35				40						45			

Leu	Gly	Ala	Ala	Asn	Cys	Glu	Ile	Met	Gly	His	Leu	Lys	Leu	Gly	Ser
	50					55					60				

Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met
 65 70 75 80
 Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp
 85 90 95
 Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val
 100 105 110
 Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile
 115 120 125
 His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
 130 135 140
 Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp
 145 150 155 160
 Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser
 165 170 175
 Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg
 180 185 190
 Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu
 195 200 205
 Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala
 210 215 220
 Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu
 225 230 235 240
 Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
 245 250 255
 Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu
 260 265 270
 Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
 275 280 285
 Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
 290 295 300
 Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
 305 310 315 320
 Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
 325 330 335
 Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
 355 360 365
 Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380
 Ala Asp Tyr Ile Ala Phe Arg Gln Asn
 385 390

<210> 23
 <211> 1179
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: nucleic acid
 sequence encoding Taxus GGPP synthase

<220>
 <221> CDS
 <222> (1)..(1179)
 <223> Computer-generated nucleic acid sequence encoding
 Taxus GGPP synthase protein

<400> 23
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 act gtt ggt tcc tat caa gaa tgc aat agt atg agg agt tgt ttt aaa 96
 Thr Val Gly Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys
 20 25 30
 ttg aca cct ttt aaa agt ttt cat gga gtg aat ttc aat gtt ccc tca 144
 Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
 35 40 45
 ctg ggt gct gct aat tgt gag att atg ggt cac ctg aaa ctt ggg tca 192
 Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser
 50 55 60
 ttg cca tat aaa caa tgt tgc gtg tca tct aaa tcc aca aaa aca atg 240
 Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met
 65 70 75 80
 gcc cag ttg gtt gat ttg gct gaa aca gag aag gcg gag gga aag gat 288
 Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp
 85 90 95
 att gaa ttt gat ttc aac gag tat atg aag tcc aag gct gtg gca gtg 336
 Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val
 100 105 110
 gat gcg gca ctg gat aag gca atc cca ctt gaa tat cct gaa aaa ata 384
 Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile
 115 120 125
 cat gaa tca atg agg tat tca ctt cta gca gga ggt aag cgc gtc agg 432
 His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
 130 135 140
 cct gct ctg tgc att gca gca tgt gag ctt gta gga ggg agt cag gac 480
 Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp
 145 150 155 160
 ctt gcc atg cca act gcc tgt gca atg gag atg att cat acc atg tct 528
 Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser
 165 170 175
 ctg att cat gat gac ttg ccg tgc atg gat aat gat gat ttc aga aga 576
 Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg
 180 185 190

ggg aag cca aca aat cac aag gtc ttt gga gag gac act gct gtt ctt 624
 Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu
 195 200 205

gca ggg gac gcc ctg ctt tca ttt gca ttt gag cat att gct gtg gct 672
 Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala
 210 215 220

aca agc aag act gtg cct agt gat agg act tta agg gtg ata tct gaa 720
 Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu
 225 230 235 240

ttg ggt aag aca ata ggc tct caa ggg ctt gta ggg ggg cag gtg gtt 768
 Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
 245 250 255

gat att aca tcc gag ggg gat gct aat gtg gac ctg aaa acc ctg gaa 816
 Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu
 260 265 270

tgg att cat ata cac aag act gct gtg ctc ttg gaa tgt tca gtt gtg 864
 Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
 275 280 285

agt gga ggg atc ctt ggt ggt gct aca gag gac gag att gcg aga att 912
 Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
 290 295 300

cgg cgg tac gcc cgg tgt gtg ggg ctt ctg ttt cag gtt gtg gat gac 960
 Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
 305 310 315 320

ata ctt gat gtc act aaa tct tct gaa gaa ttg gga aag act gca gga 1008
 Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
 325 330 335

aag gat ttg ctt act gat aag gct act tat ccc aag ttg atg ggc ctg 1056
 Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350

gag aaa gca aaa gaa ttt gcc gct gaa ttg gcg acg aga gcc aag gaa 1104
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
 355 360 365

gag ctg tca tcc ttt gat cag ata aag gct gca cct ttg ttg ggt ctt 1152
 Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380

gca gat tac att gca ttc agg caa aac 1179
 Ala Asp Tyr Ile Ala Phe Arg Gln Asn
 385 390

<210> 24

<211> 393

<212> PRT

<213> Artificial Sequence

<400> 24

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Thr Val Gly Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys

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Leu	Thr	Pro	Phe	Lys	Ser	Phe	His	Gly	Val	Asn	Phe	Asn	Val	Pro	Ser
		35					40					45			
Leu	Gly	Ala	Ala	Asn	Cys	Glu	Ile	Met	Gly	His	Leu	Lys	Leu	Gly	Ser
	50					55					60				
Leu	Pro	Tyr	Lys	Gln	Cys	Ser	Val	Ser	Ser	Lys	Ser	Thr	Lys	Thr	Met
	65					70					75				80
Ala	Gln	Leu	Val	Asp	Leu	Ala	Glu	Thr	Glu	Lys	Ala	Glu	Gly	Lys	Asp
				85					90					95	
Ile	Glu	Phe	Asp	Phe	Asn	Glu	Tyr	Met	Lys	Ser	Lys	Ala	Val	Ala	Val
			100					105					110		
Asp	Ala	Ala	Leu	Asp	Lys	Ala	Ile	Pro	Leu	Glu	Tyr	Pro	Glu	Lys	Ile
		115					120					125			
His	Glu	Ser	Met	Arg	Tyr	Ser	Leu	Leu	Ala	Gly	Gly	Lys	Arg	Val	Arg
						135					140				
Pro	Ala	Leu	Cys	Ile	Ala	Ala	Cys	Glu	Leu	Val	Gly	Gly	Ser	Gln	Asp
	145					150					155				160
Leu	Ala	Met	Pro	Thr	Ala	Cys	Ala	Met	Glu	Met	Ile	His	Thr	Met	Ser
				165					170					175	
Leu	Ile	His	Asp	Asp	Leu	Pro	Cys	Met	Asp	Asn	Asp	Asp	Phe	Arg	Arg
			180					185					190		
Gly	Lys	Pro	Thr	Asn	His	Lys	Val	Phe	Gly	Glu	Asp	Thr	Ala	Val	Leu
		195					200					205			
Ala	Gly	Asp	Ala	Leu	Leu	Ser	Phe	Ala	Phe	Glu	His	Ile	Ala	Val	Ala
	210					215					220				
Thr	Ser	Lys	Thr	Val	Pro	Ser	Asp	Arg	Thr	Leu	Arg	Val	Ile	Ser	Glu
	225					230					235				240
Leu	Gly	Lys	Thr	Ile	Gly	Ser	Gln	Gly	Leu	Val	Gly	Gly	Gln	Val	Val
			245						250					255	
Asp	Ile	Thr	Ser	Glu	Gly	Asp	Ala	Asn	Val	Asp	Leu	Lys	Thr	Leu	Glu
			260					265					270		
Trp	Ile	His	Ile	His	Lys	Thr	Ala	Val	Leu	Leu	Glu	Cys	Ser	Val	Val
		275					280					285			
Ser	Gly	Gly	Ile	Leu	Gly	Gly	Ala	Thr	Glu	Asp	Glu	Ile	Ala	Arg	Ile
	290					295					300				
Arg	Arg	Tyr	Ala	Arg	Cys	Val	Gly	Leu	Leu	Phe	Gln	Val	Val	Asp	Asp
	305					310					315				320
Ile	Leu	Asp	Val	Thr	Lys	Ser	Ser	Glu	Glu	Leu	Gly	Lys	Thr	Ala	Gly
				325					330					335	
Lys	Asp	Leu	Leu	Thr	Asp	Lys	Ala	Thr	Tyr	Pro	Lys	Leu	Met	Gly	Leu
			340					345					350		
Glu	Lys	Ala	Lys	Glu	Phe	Ala	Ala	Glu	Leu	Ala	Thr	Arg	Ala	Lys	Glu
		355					360					365			

Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380

Ala Asp Tyr Ile Ala Phe Arg Gln Asn
 385 390

<210> 25

<211> 1179

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: nucleic acid
 sequence encoding Taxus GGPP synthase

<220>

<221> CDS

<222> (1)..(1179)

<223> Computer-generated nucleic acid sequence encoding
 Taxus GGPP synthase protein

<400> 25

atg gct tac acg gca atg gca gca ggg acc caa agc ttg caa ctc cgc 48
 Met Ala Tyr Thr Ala Met Ala Ala Gly Thr Gln Ser Leu Gln Leu Arg
 1 5 10 15

act gtt gct tcc tat caa gac tgc aat agt atg agg agt tgt ttt aaa 96
 Thr Val Ala Ser Tyr Gln Asp Cys Asn Ser Met Arg Ser Cys Phe Lys
 20 25 30

ttg aca cct ttt aaa agt ttt cat gga gtg aat ttc aat gtt ccc tca 144
 Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
 35 40 45

ctg ggt gct gct aat tgt gag att atg ggt cac ctg aaa ctt ggg tca 192
 Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser
 50 55 60

ttg cca tat aaa caa tgt tcg gtg tca tct aaa tcc aca aaa aca atg 240
 Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met
 65 70 75 80

gcc cag ttg gtt gat ttg gct gaa aca gag aag gcg gag gga aag gat 288
 Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp
 85 90 95

att gaa ttt gat ttc aac gag tat atg aag tcc aag gct gtg gca gtg 336
 Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val
 100 105 110

gat gcg gca ctg gat aag gca atc cca ctt gaa tat cct gaa aaa ata 384
 Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile
 115 120 125

cat gaa tca atg agg tat tca ctt cta gca gga ggt aag cgc gtc agg 432
 His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
 130 135 140

cct gct ctg tgc att gca gca tgt gag ctt gta gga ggg agt cag gac 480
 Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp
 145 150 155 160

ctt gcc atg cca act gcc tgt gca atg gag atg att cat acc atg tct 528
 Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser
 165 170 175

ctg att cat gat gac ttg ccg tgc atg gat aat gat gat ttc aga aga 576
 Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg
 180 185 190

ggg aag cca aca aat cac aag gtc ttt gga gag gac act gct gtt ctt 624
 Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu
 195 200 205

gca ggg gac gcc ctg ctt tca ttt gca ttt gag cat att gct gtg gct 672
 Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala
 210 215 220

aca agc aag act gtg cct agt gat agg act tta agg gtg ata tct gaa 720
 Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu
 225 230 235 240

ttg ggt aag aca ata ggc tct caa ggg ctt gta ggg ggg cag gtg gtt 768
 Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
 245 250 255

gat att aca tcc gag ggg gat gct aat gtg gac ctg aaa acc ctg gaa 816
 Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu
 260 265 270

tgg att cat ata cac aag act gct gtg ctc ttg gaa tgt tca gtt gtg 864
 Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
 275 280 285

agt gga ggg atc ctt ggt ggt gct aca gag gac gag att gcg aga att 912
 Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
 290 295 300

cgg cgg tac gcc cgg tgt gtg ggg ctt ctg ttt cag gtt gtg gat gac 960
 Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
 305 310 315 320

ata ctt gat gtc act aaa tct tct gaa gaa ttg gga aag act gca gga 1008
 Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
 325 330 335

aag gat ttg ctt act gat aag gct act tat ccc aag ttg atg ggc ctg 1056
 Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350

gag aaa gca aaa gaa ttt gcc gct gaa ttg gcg acg aga gcc aag gaa 1104
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
 355 360 365

gag ctg tca tcc ttt gat cag ata aag gct gca cct ttg ttg ggt ctt 1152
 Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380

gca gat tac att gca ttc agg caa aac 1179
 Ala Asp Tyr Ile Ala Phe Arg Gln Asn
 385 390

<210> 26

<211> 393

<212> PRT

<213> Artificial Sequence

<400> 26

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Thr Val Ala Ser Tyr Gln Asp Cys Asn Ser Met Arg Ser Cys Phe Lys
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Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
      35           40           45

Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser
      50           55           60

Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met
      65           70           75           80

Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp
      85           90           95

Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val
      100          105          110

Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile
      115          120          125

His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
      130          135          140

Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp
      145          150          155          160

Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser
      165          170          175

Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg
      180          185          190

Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu
      195          200          205

Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala
      210          215          220

Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu
      225          230          235          240

Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
      245          250          255

Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu
      260          265          270

Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
      275          280          285

Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
      290          295          300

Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
      305          310          315          320

Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly

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325 330 335
 Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
 355 360 365
 Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380
 Ala Asp Tyr Ile Ala Phe Arg Gln Asn
 385 390

<210> 27

<211> 393

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Taxus GGPP
 synthase protein variant

<220>

<221> VARIANT

<222> (1)..(393)

<223> Computer-generated Taxus GGPP synthase protein
 variant

<400> 27

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 20 25 30
 Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
 35 40 45
 Leu Ala Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser
 50 55 60
 Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met
 65 70 75 80
 Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp
 85 90 95
 Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val
 100 105 110
 Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile
 115 120 125
 His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
 130 135 140
 Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp
 145 150 155 160
 Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser
 165 170 175

Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg
 180 185 190
 Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu
 195 200 205
 Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala
 210 215 220
 Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu
 225 230 235 240
 Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
 245 250 255
 Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu
 260 265 270
 Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
 275 280 285
 Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
 290 295 300
 Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
 305 310 315 320
 Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
 325 330 335
 Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
 355 360 365
 Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380
 Ala Asp Tyr Ile Ala Phe Arg Gln Asn
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<211> 393

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Taxus GGPP
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<221> VARIANT

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<223> Computer-generated Taxus GGPP synthase protein
 variant

<400> 28

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Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys
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Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
 35 40 45
 Leu Gly Gly Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser
 50 55 60
 Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met
 65 70 75 80
 Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp
 85 90 95
 Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val
 100 105 110
 Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile
 115 120 125
 His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
 130 135 140
 Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp
 145 150 155 160
 Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser
 165 170 175
 Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg
 180 185 190
 Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu
 195 200 205
 Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala
 210 215 220
 Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu
 225 230 235 240
 Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
 245 250 255
 Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu
 260 265 270
 Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
 275 280 285
 Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
 290 295 300
 Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
 305 310 315 320
 Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
 325 330 335
 Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
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Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380

Ala Asp Tyr Ile Ala Phe Arg Gln Asn
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<210> 29

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<212> PRT

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<222> (1)..(393)

<223> Computer-generated Taxus GGPP synthase protein
 variant

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Met Ala Tyr Thr Ala Met Ala Ala Gly Thr Gln Ser Leu Gln Leu Arg
 1 5 10 15

Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys
 20 25 30

Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
 35 40 45

Leu Gly Ala Ala Asn Cys Asp Ile Met Gly His Leu Lys Leu Gly Ser
 50 55 60

Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met
 65 70 75 80

Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp
 85 90 95

Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val
 100 105 110

Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile
 115 120 125

His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
 130 135 140

Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp
 145 150 155 160

Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser
 165 170 175

Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg
 180 185 190

Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu
 195 200 205

Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala
 210 215 220

Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu
 225 230 235 240
 Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
 245 250 255
 Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu
 260 265 270
 Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
 275 280 285
 Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
 290 295 300
 Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
 305 310 315 320
 Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
 325 330 335
 Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
 355 360 365
 Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380
 Ala Asp Tyr Ile Ala Phe Arg Gln Asn
 385 390

<210> 30
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 <213> Artificial Sequence

<220>
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 synthase protein variant

<220>
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 <222> (1)..(393)
 <223> Computer-generated Taxus GGPP synthase protein
 variant

<400> 30
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 Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys
 20 25 30
 Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
 35 40 45
 Leu Gly Ala Ala Asn Cys Glu Ile Met Ala His Leu Lys Leu Gly Ser
 50 55 60
 Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met

65	70	75	80
Ala Gln Leu Val Asp 85	Leu Ala Glu Thr Glu 90	Lys Ala Glu Gly Lys 95	Asp
Ile Glu Phe Asp 100	Phe Asn Glu Tyr Met 105	Lys Ser Lys Ala Val 110	Ala Val
Asp Ala Ala Leu Asp 115	Lys Ala Ile Pro Leu 120	Glu Tyr Pro Glu Lys 125	Ile
His Glu Ser Met Arg 130	Tyr Ser Leu Leu Ala 135	Gly Gly Lys Arg Val 140	Arg
Pro Ala Leu Cys Ile 145	Ala Ala Cys Glu Leu 150	Val Gly Gly Ser Gln 155	Asp 160
Leu Ala Met Pro Thr 165	Ala Cys Ala Met Glu 170	Met Ile His Thr Met 175	Ser
Leu Ile His Asp 180	Asp Leu Pro Cys Met 185	Asn Asp Asp Phe Arg 190	Arg
Gly Lys Pro Thr 195	Asn His Lys Val Phe 200	Gly Glu Asp Thr Ala 205	Val Leu
Ala Gly Asp Ala Leu 210	Leu Ser Phe Ala Phe 215	Glu His Ile Ala Val 220	Ala
Thr Ser Lys Thr Val 225	Pro Ser Asp Arg Thr 230	Leu Arg Val Ile Ser 235	Glu 240
Leu Gly Lys Thr 245	Ile Gly Ser Gln Gly 250	Leu Val Gly Gly Gln 255	Val
Asp Ile Thr Ser 260	Glu Gly Asp Ala Asn 265	Val Asp Leu Lys Thr 270	Leu Glu
Trp Ile His Ile His 275	Lys Thr Ala Val Leu 280	Leu Glu Cys Ser Val 285	Val
Ser Gly Gly Ile Leu 290	Gly Gly Ala Thr Glu 295	Asp Glu Ile Ala Arg 300	Ile
Arg Arg Tyr Ala Arg 305	Cys Val Gly Leu Leu 310	Phe Gln Val Val Asp 315	Asp 320
Ile Leu Asp Val Thr 325	Lys Ser Ser Glu Glu 330	Leu Gly Lys Thr Ala 335	Gly
Lys Asp Leu Leu Thr 340	Asp Lys Ala Thr Tyr 345	Pro Lys Leu Met Gly 350	Leu
Glu Lys Ala Lys Glu 355	Phe Ala Ala Glu Leu 360	Ala Thr Arg Ala Lys 365	Glu
Glu Leu Ser Ser Phe 370	Asp Gln Ile Lys Ala 375	Ala Pro Leu Leu Gly 380	Leu
Ala Asp Tyr Ile Ala 385	Phe Arg Gln Asn		

<211> 393
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: GGPP synthase protein variant

<220>
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 <223> Computer-generated Taxus GGPP synthase protein variant

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 Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys
 20 25 30
 Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
 35 40 45
 Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Arg Leu Gly Ser
 50 55 60
 Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met
 65 70 75 80
 Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp
 85 90 95
 Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val
 100 105 110
 Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile
 115 120 125
 His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
 130 135 140
 Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp
 145 150 155 160
 Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser
 165 170 175
 Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg
 180 185 190
 Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu
 195 200 205
 Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala
 210 215 220
 Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu
 225 230 235 240
 Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
 245 250 255
 Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu

260 265 270

Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
275 280 285

Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
290 295 300

Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
305 310 315 320

Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
325 330 335

Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
340 345 350

Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
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Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
370 375 380

Ala Asp Tyr Ile Ala Phe Arg Gln Asn
385 390

<210> 32

<211> 393

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: variant of
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<220>

<221> VARIANT

<222> (1)..(393)

<223> Computer-generated variant of Taxus GGPP synthase
protein

<400> 32

Met Ala Tyr Thr Ala Met Ala Ala Gly Thr Gln Ser Leu Gln Leu Arg
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Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys
20 25 30

Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
35 40 45

Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser
50 55 60

Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Arg Ser Thr Lys Thr Met
65 70 75 80

Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp
85 90 95

Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val
100 105 110

Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile
 115 120 125
 His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
 130 135 140
 Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp
 145 150 155 160
 Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser
 165 170 175
 Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg
 180 185 190
 Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu
 195 200 205
 Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala
 210 215 220
 Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu
 225 230 235 240
 Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
 245 250 255
 Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu
 260 265 270
 Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
 275 280 285
 Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
 290 295 300
 Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
 305 310 315 320
 Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
 325 330 335
 Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
 355 360 365
 Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380
 Ala Asp Tyr Ile Ala Phe Arg Gln Asn
 385 390

<210> 33

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<212> PRT

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 <223> Description of Artificial Sequence: Taxus GGPP
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<220>

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<222> (1)..(393)

<223> Computer-generated Taxus GGPP synthase variant

<400> 33

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Met Ala Tyr Thr Ala Met Ala Ala Gly Thr Gln Ser Leu Gln Leu Arg
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Thr Val Ala Ser Tyr Gln Glu Cys Asn Ser Met Arg Ser Cys Phe Lys
          20           25           30

Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
          35           40           45

Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser
 50           55           60

Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Arg Ser Thr Lys Thr Met
 65           70           75

Ala Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp
          85           90           95

Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val
          100          105          110

Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile
          115          120          125

His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
          130          135          140

Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp
          145          150          155          160

Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser
          165          170          175

Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg
          180          185          190

Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu
          195          200          205

Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala
          210          215          220

Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu
          225          230          235          240

Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
          245          250          255

Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu
          260          265          270

Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
          275          280          285

Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
          290          295          300

Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp

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305 310 315 320
 Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
 325 330 335
 Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
 355 360 365
 Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380
 Ala Asp Tyr Ile Ala Phe Arg Gln Asn
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<210> 34

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<212> PRT

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<223> Description of Artificial Sequence: Taxus GGPP synthase protein variant

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<222> (1)..(393)

<223> Computer-generated Taxus GGPP synthase protein variant

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 Leu Thr Pro Phe Lys Ser Phe His Gly Val Asn Phe Asn Val Pro Ser
 35 40 45
 Leu Gly Ala Ala Asn Cys Glu Ile Met Gly His Leu Lys Leu Gly Ser
 50 55 60
 Leu Pro Tyr Lys Gln Cys Ser Val Ser Ser Lys Ser Thr Lys Thr Met
 65 70 75 80
 Gly Gln Leu Val Asp Leu Ala Glu Thr Glu Lys Ala Glu Gly Lys Asp
 85 90 95
 Ile Glu Phe Asp Phe Asn Glu Tyr Met Lys Ser Lys Ala Val Ala Val
 100 105 110
 Asp Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile
 115 120 125
 His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
 130 135 140
 Pro Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp
 145 150 155 160

Leu Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser
 165 170 175
 Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg
 180 185 190
 Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu
 195 200 205
 Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala
 210 215 220
 Thr Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu
 225 230 235 240
 Leu Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val
 245 250 255
 Asp Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu
 260 265 270
 Trp Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val
 275 280 285
 Ser Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile
 290 295 300
 Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp
 305 310 315 320
 Ile Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly
 325 330 335
 Lys Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
 340 345 350
 Glu Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu
 355 360 365
 Glu Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu
 370 375 380
 Ala Asp Tyr Ile Ala Phe Arg Gln Asn
 385 390

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/25262**A. CLASSIFICATION OF SUBJECT MATTER**IPC(6) : C12N 9/00, 1/20, 15/00; C07H 21/04; C07K 1/00
US CL : 435/183, 252.3, 320.1; 530/350; 536/23.2, 23.6

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/183, 252.3, 320.1; 530/350; 536/23.2, 23.6

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

STN FILES : CAPLUS, MEDLINE, BIOSIS, EMBASE, USPATFULL. WEST. Search terms : geranylgeranyl diphosphate synthase? and Taxus, and (rna or dna or nucleic acid? or gene?, etc.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	*Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	BONK, M. et al. Chloroplast Import of Four Carotenoid Biosynthetic Enzymes in vitro Reveals Differential Fates prior to Membrane Binding and Oligomeric Assembly. Eur. J. Biochem. 1997. Vol. 247. pages 942-950, especially page 942.	1-18

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
B earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

30 DECEMBER 1999

Date of mailing of the international search report

19 JAN 2000

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

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Authorized officer

TEKCHAND SAIDHA

Telephone No. (703) 308-0196